GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:59 ; Search time 18 Seconds
(without alignments)
1638.370 Million cell updates/sec

Title: US-09-806-194-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3651	100.0	697	4	US-09-548-372D-16	Sequence 16, Appl
2	3651	100.0	697	4	US-09-548-367D-16	Sequence 16, Appl
3	3651	100.0	697	4	US-09-551-853D-16	Sequence 16, Appl
4	3646	99.9	697	4	US-09-548-372D-20	Sequence 20, Appl
5	3646	99.9	697	4	US-09-548-367D-20	Sequence 20, Appl
6	3646	99.9	697	4	US-09-551-853D-20	Sequence 20, Appl
7	3643	99.8	697	4	US-09-548-372D-18	Sequence 18, Appl
8	3643	99.8	697	4	US-09-548-367D-18	Sequence 18, Appl
9	3643	99.8	697	4	US-09-551-853D-18	Sequence 18, Appl
10	3641	99.7	695	1	US-08-123-702-2	Sequence 2, Appli
11	3641	99.7	695	2	US-08-104-165-1	Sequence 1, Appli
12	3641	99.7	695	3	US-08-464-250-1	Sequence 1, Appli
13	3641	99.7	695	4	US-08-464-250-1	Sequence 1, Appli
14	3641	99.7	695	4	US-09-458-481B-7	Sequence 7, Appli
15	3641	99.7	695	4	US-09-458-481B-8	Sequence 8, Appli
16	3641	99.7	695	4	US-09-548-372D-10	Sequence 10, Appl
17	3641	99.7	695	4	US-09-548-367D-10	Sequence 10, Appl
18	3641	99.7	695	4	US-09-551-853D-10	Sequence 10, Appl
19	3641	99.7	695	6	5218100-2	Patent No. 5218100
20	3636	99.6	695	4	US-09-548-372D-14	Sequence 14, Appl
21	3636	99.6	695	4	US-09-548-367D-14	Sequence 14, Appl
22	3636	99.6	695	4	US-09-551-853D-14	Sequence 14, Appl
23	3635	99.6	694	1	US-08-339-152A-18	Sequence 18, Appl
24	3635	99.6	694	2	US-08-007-999B-5	Sequence 5, Appli
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26	3633	99.5	695	4	US-09-548-372D-12	Sequence 12, Appl
27	3633	99.5	695	4	US-09-548-367D-12	Sequence 12, Appl
28	3633	99.5	695	4	US-09-551-853D-12	Sequence 12, Appl
29	3629	99.4	695	1	US-08-371-930-27	Sequence 27, Appl
30	3629	99.4	695	5	PCT-US94-01712-27	Sequence 27, Appl
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35	3602	98.7	751	1	US-08-123-702-4	Sequence 4, Appli
36	3602	98.7	751	2	US-08-104-165-2	Sequence 2, Appli
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38	3602	98.7	751	2	US-08-422-333-21	Sequence 21, Appl
39	3602	98.7	751	3	US-08-464-250-2	Sequence 2, Appli
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41	3602	98.7	751	4	US-08-832-867-5	Sequence 5, Appli
42	3602	98.7	751	4	US-09-548-372D-57	Sequence 57, Appl
43	3602	98.7	751	4	US-09-548-367D-57	Sequence 57, Appl
44	3602	98.7	751	4	US-09-551-853D-57	Sequence 57, Appl
45	3602	98.7	751	6	5187153-2	Patent No. 5187153

ALIGNMENTS

RESULT 1
US-09-548-372D-16
; Sequence 16, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapines
US-09-548-372D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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; Sequence 16, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapines
US-09-548-367D-16

  Query Match           100.0%;  Score 3651;  DB 4;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-264;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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RESULT 3
US-09-551-853D-16
; Sequence 16, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapines
US-09-551-853D-16

  Query Match           100.0%;  Score 3651;  DB 4;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-264;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

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RESULT 4
US-09-548-372D-20
; Sequence 20, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-20

  Query Match           99.9%;  Score 3646;  DB 4;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 3.7e-264;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 5
US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
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; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-20

Query Match 99.9%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.7e-264;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 6
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-20

Query Match 99.9%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 3.7e-264;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 7
US-09-548-372D-18
; Sequence 18, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF

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;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-18

  Query Match             99.8%;  Score 3643;  DB 4;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 6.2e-264;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHILKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 8
US-09-548-367D-18
; Sequence 18, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-18

  Query Match             99.8%;  Score 3643;  DB 4;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 6.2e-264;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
US-09-551-853D-18
; Sequence 18, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/5280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-18

  Query Match           99.8%;  Score 3643;  DB 4;  Length 697;
  Best Local Similarity  99.7%;  Pred. No. 6.2e-264;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 10
US-08-123-702-2
; Sequence 2, Application US/08123702
; Patent No. 5604131
;  GENERAL INFORMATION:
;    APPLICANT:  Wadsworth, Samuel
;    APPLICANT:  Snyder, Benjamin
;    APPLICANT:  Reddy, Vermuri, B.
;    APPLICANT:  Wei, Chamer
;    TITLE OF INVENTION:  A cDNA Genomic Hybrid Sequence Encoding APP770
; Patent No. 5604131
;    TITLE OF INVENTION:  Containing a Genomic DNA Insert of the KI and OX-2 Regic
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  GA
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/123,702
;      FILING DATE:  17-SEPT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  TSI121
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404)-873-8794
;      TELEFAX:  (404)-873-8795
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-123-702-2

  Query Match           99.7%;  Score 3641;  DB 1;  Length 695;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 11
US-08-104-165-1
; Sequence 1, Application US/08104165
; Patent No. 5877015
;  GENERAL INFORMATION:
;    APPLICANT:  HARDY, John Anthony
;    APPLICANT:  GOATE, Alison Mary
;    APPLICANT:  MULLAN, Michael John
;    APPLICANT:  CHARTIER-HARLIN, Marie-Christine
;    APPLICANT:  OWEN, Michael John
;    TITLE OF INVENTION:  Test and Model for Alzheimer's Disease
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/104,165
;      FILING DATE:  21-JAN-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  9101507.8
;      FILING DATE:  21-JAN-1991
;      APPLICATION NUMBER:  9118445.7
;      FILING DATE:  28-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joe
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  16163-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-104-165-1

  Query Match             99.7%;  Score 3641;  DB 2;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 12
US-08-464-250-1
; Sequence 1, Application US/08464250
; Patent No. 6107542
;  GENERAL INFORMATION:
;    APPLICANT:  HARDY, John Anthony
;    APPLICANT:  GOATE, Alison Mary
```

```
;    APPLICANT:  MULLAN, Michael John
;    APPLICANT:  CHARTIER-HARLIN, Marie-Christine
;    APPLICANT:  OWEN, Michael John
;    TITLE OF INVENTION:  Test and Model for Alzheimer's Disease
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,250
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/104,165
;      FILING DATE:  21-JAN-1992
;      APPLICATION NUMBER:  9101307.8
;      FILING DATE:  21-JAN-1991
;      APPLICATION NUMBER:  9118445.7
;      FILING DATE:  28-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joe
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  16163-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-250-1

  Query Match             99.7%;  Score 3641;  DB 3;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 13
US-08-464-250-1
; Sequence 1, Application US/08464250
; Patent No. 6300540
;   GENERAL INFORMATION:
;        APPLICANT: HARDY, John Anthony
;                   GOATE, Alison Mary
;                   MULLAN, Michael John
;                   CHARTIER-HARLIN, Marie-Christine
;                   OWEN, Michael John
;        TITLE OF INVENTION: Test and Model for Alzheimer's Disease
;        NUMBER OF SEQUENCES: 44
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend Khourie and Crew
;             STREET: 379 Lytton Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: US
;             ZIP: 94301
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy Disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/464,250
;             FILING DATE: 05-Jun-1995
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/104,165
;             FILING DATE: 21-JAN-1992
;             APPLICATION NUMBER: 9101307.8
;             FILING DATE: 21-JAN-1991
;             APPLICATION NUMBER: 9118445.7
;             FILING DATE: 28-AUG-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 16163-000100
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 326-2400
;             TELEFAX: (415) 326-2422
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 695 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-464-250-1
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  Query Match             99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHILKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 14
US-09-458-481B-7
; Sequence 7, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
;  APPLICANT: KUMAR, Vijaya B.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
;  FILE REFERENCE: 16153-9250
;  CURRENT APPLICATION NUMBER: US/09/458,481B
;  CURRENT FILING DATE:  1999-12-09
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Monkey
US-09-458-481B-7

  Query Match             99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 15
US-09-458-481B-8
; Sequence 8, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
;  APPLICANT: KUMAR, Vijaya B.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
;  FILE REFERENCE: 16153-9250
;  CURRENT APPLICATION NUMBER: US/09/458,481B
;  CURRENT FILING DATE:  1999-12-09
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-458-481B-8

  Query Match             99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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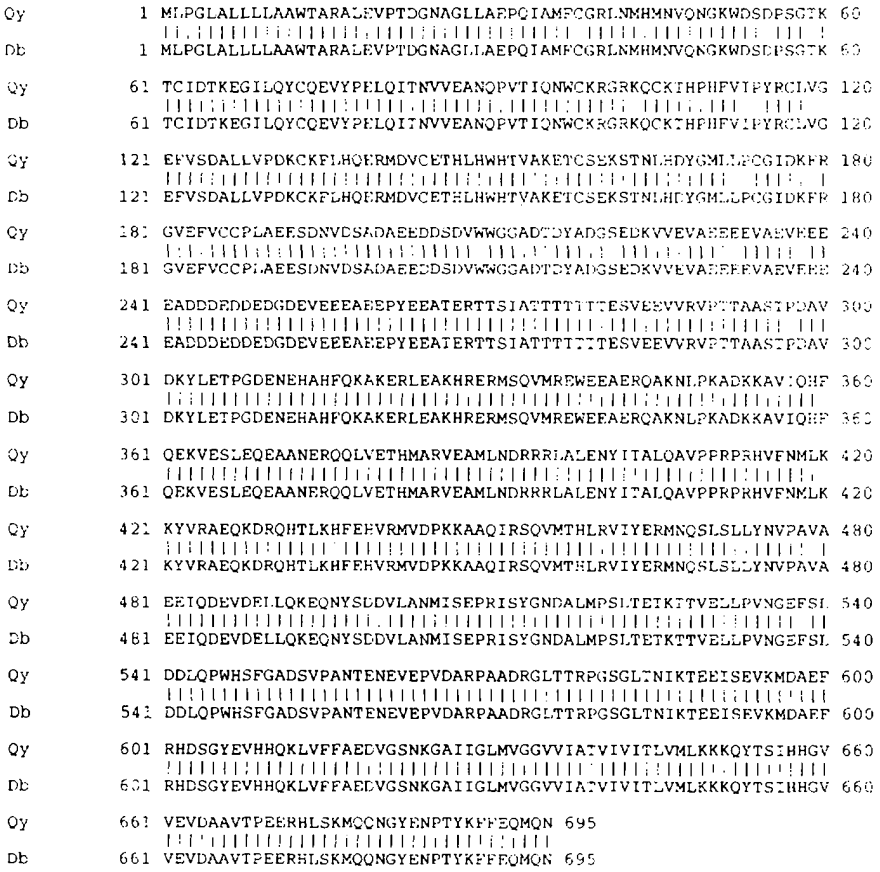

Search completed: October 2, 2003, 14:03:34
Job time : 20 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:09 ; Search time 38.3333 Seconds
(without alignments)
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Title: US-09-806-194-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3651	100.0	697	21	AAY88428	Human APP696-KK am
2	3651	100.0	697	22	AAE10635	Human amyloid prot
3	3651	100.0	697	22	AAE06865	Human amyloid prec
4	3651	100.0	697	22	AAU06609	Human Amyloid prec
5	3651	100.0	697	22	AAU07208	Human beta-amyloid
6	3651	100.0	697	22	AAE02587	Human amyloid prec
7	3651	100.0	697	23	ABB78596	Human APP695-KK pr
8	3646	99.9	697	21	AAY88430	Human APP695-VF-KK
9	3646	99.9	697	22	AAE10637	Human amyloid prot
10	3646	99.9	697	22	AAE06867	Human amyloid prec
11	3646	99.9	697	22	AAU06611	Human Amyloid prec
12	3646	99.9	697	22	AAU07210	Human beta-amyloid
13	3646	99.9	697	22	AAE02589	Human amyloid prec
14	3646	99.9	697	23	ABB78598	Human APP695-VF-KK
15	3643	99.8	697	21	AAY88429	Human APPSW-KK ami
16	3643	99.8	697	22	AAE10636	Human amyloid prot
17	3643	99.8	697	22	AAE06866	Human amyloid prec
18	3643	99.8	697	22	AAU06610	Human Amyloid prec
19	3643	99.8	697	22	AAU07209	Human beta-amyloid
20	3643	99.8	697	22	AAE02588	Human amyloid prec
21	3643	99.8	697	23	ABB78597	Human APP695-SW-KK
22	3641	99.7	695	9	AAP81692	Sequence of human
23	3641	99.7	695	13	AAR26338	APP695. Homo sapi
24	3641	99.7	695	19	AAY20233	Human beta-amyloid
25	3641	99.7	695	20	AAY07221	Amyloid precursor
26	3641	99.7	695	21	AAY88434	Human APP695 amino
27	3641	99.7	695	21	AAY44705	Human beta amyloid
28	3641	99.7	695	22	AAE10632	Human wild-type am
29	3641	99.7	695	22	AAE06862	Human wild-type am
30	3641	99.7	695	22	AAU06606	Human Amyloid prec
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33	3641	99.7	695	23	ABB78593	Human APP695 prote
34	3641	99.7	695	23	AAG68315	Human amyloid prec
35	3641	99.7	695	24	ABB99604	Amino acid sequenc
36	3638	99.6	695	20	AAY49690	Human beta amyloid
37	3636	99.6	695	18	AAW19498	APP695 mutant A-be
38	3636	99.6	695	18	AAW19484	APP695 mutant A-be
39	3636	99.6	695	18	AAW19495	APP695 mutant A-be
40	3636	99.6	695	18	AAW19481	APP695 mutant A-be
41	3636	99.6	695	21	AAY88436	Human APP695-VF am
42	3636	99.6	695	22	AAE10634	Human amyloid prot
43	3636	99.6	695	22	AAE06864	Human amyloid prec
44	3636	99.6	695	22	AAU06608	Human Amyloid prec
45	3636	99.6	695	22	AAU07207	Human beta-amyloid

ALIGNMENTS

RESULT 1
AAY88428
ID AAY88428 standard; Protein; 697 AA.
XX
AC AAY88428;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human APP696-KK amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APP696-KK.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15665.
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

PT the beta secretase site to produce amyloid beta peptide -
XX
PS Claim 132; Page 137-141; 183pp; English.
XX
CC This sequence represents a modified version of the human amyloid
CC precursor protein (APP) amino acid sequence. The sequence is used in an
CC example of the method of the invention, to show that modification of APP
CC increases beta amyloid protein processing. The invention relates to a
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC amyloid precursor protein (APP). The protease contains a sequence
CC encoding the amino acid sequence DTG and a sequence encoding DSG or LTG
CC separated by 100-300 amino acids. When mutated the APP gene causes an
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC nucleotide sequence, and a cell line comprising the vector. Methods for
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease.
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 21; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.7e-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy 241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db 241 EADDDFDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

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Qy 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

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Db 481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

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Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 2
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ID AAE10635 standard; Protein; 697 AA.
XX
AC AAE10635;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human amyloid protein precursor 695-KK (APP695-KK) isoform.
XX
KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP695-KK;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR N-PSDB; AAD17871.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
PS Example 6; Page 114-116; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-KK (APP695-KK) isoform which is obtained by
CC the addition of two Lys residues (KK motif) at the C-terminus of
CC APP695 protein.
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 22; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.7e-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300
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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 3
AAE06865
ID   AAE06865 standard; Protein; 697 AA.
XX
AC   AAE06865;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-KK (APP695-KK) isoform.
XX
KW   Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; gene therapy; APP695-KK; mutant;
KW   mutein.
XX
OS   Homo sapiens.
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00799.
XX
PR   09-MAY-2001; 2001WO-IB00799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-483072/52.
DR   N-PSDB; AAD13027.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting
CC   Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC   blots. The present sequence is modified human amyloid precursor
CC   protein 695-KK (APP695-KK) isoform. APP695-KK isoform is obtained by
CC   addition of two Lys residues (KK motif) at the C-terminal end of APP695
CC   isoform.
XX
SQ   Sequence   697 AA;

  Query Match           100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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```
Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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```
RESULT 4
AAU06609
ID   AAU06609 standard; Protein; 697 AA.
XX
AC   AAU06609;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-KK.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-KK; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 696..697
FT                   /note= "2 Extra Lys residues added compared to
FT                   wild-type APP695"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00798.
XX
PR   09-MAY-2001; 2001WO-IB00798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502549/55.
DR   N-PSDB; AAS11523.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp
CC   proteins and vectors expressing them, and a polypeptide (isoform of
CC   amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC   APP or its fragment containing an APP cleavage site recognizable by a
CC   mammalian beta-secretase, and further comprising two lysine residues at
CC   the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC   APP fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and
CC   amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease.
CC   APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC   is associated with increased levels of Abeta processing is useful in
CC   assays relating the Alzheimer's research. The expression vector is useful
CC   for recombinantly expressing APP. Nucleic acids that hybridise to
CC   Asp oligonucleotides are  useful as probes or primers. The probes are
CC   useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence is the human
CC   APP695 mutant, APP695-KK which has 2 extra Lys residues added at
CC   the C-terminus compared to the wild-type APP695. The mutation alters the
CC   specificity of the APP gamma-secretase activity and increases the rate
CC   of processing of the amyloid Abeta peptide.
XX
SQ   Sequence   697 AA;
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  Query Match             100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTIESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTIESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
```

```
Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||:|||||||:|||||||| |||||:||||||'||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 5
AAU07208
ID   AAU07208 standard; Protein; 697 AA.
XX
AC   AAU07208;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human beta-amyloid protein precursor, APP695-KK.
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; APP695-KK.
XX
OS   Homo sapiens.
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00797.
XX
PR   09-MAY-2001; 2001WO-IB00797.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-502548/55.
DR   N-PSDB; AAS11708.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing
CC   an APP cleavage site recognisable by a mammalian beta-secretase, and
CC   further comprising two lysine residues at the carboxyl terminus of the
CC   amino acid sequence of the mammalian APP or APP fragment. The
CC   polypeptides are used for assaying for modulators of beta-secretase
CC   activity; identifying agents that inhibit the APP processing activity
CC   of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC   modulate the activity of Asp2; and for reducing cellular production of
CC   amyloid beta (Abeta) from APP. Agents identified by the above methods
CC   are useful for treating Alzheimer's disease; and for identifying
CC   modulators of amyloid-beta (Abeta) peptide production, for use in
CC   designing therapeutics for the treatment or prevention of Alzheimer's
CC   disease. Probes and primers derived from Asp nucleic acid sequences
CC   are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence represents the
CC   amino acid sequence of human amyloid protein precursor, APP695-KK,
CC   used in the method of the invention.
XX
SQ   Sequence   697 AA;

  Query Match             100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLIETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||:|||||||||||||||||||||||||||||:|||||||||| ||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||:|||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 6
AAE02587
ID   AAE02587 standard; Protein; 697 AA.
XX
AC   AAE02587;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-KK (APP695-KK).
XX
KW   Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
KW   therapy; Alzheimer's disease; antialzheimer's.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26080.
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XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M, Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   N-PSDB; AAD06745.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Example 6; Page 143-145; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human APP695-KK. This
CC   sequence contains two carboxy-terminal lysine residues.
XX
SQ   Sequence   697 AA;

  Query Match             100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 7
ABB78596
ID   ABB78596 standard; Protein; 697 AA.
XX
AC   ABB78596;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human APP695-KK protein sequence SEQ ID NO:16.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW   proteolytic; amyloid precursor protein; APP.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-0025934.
XX
PR   23-SEP-1999;   99US-155493P.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-169232P.
PR   22-SEP-2000; 2000GB-0023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ, Gurney M;
XX
DR   WPI; 2002-396337/43.
DR   N-PSDB; ABL52463.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect
PT   aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT   disease -
XX
PS   Example 6; Page 114-116; 182pp; English.
XX
CC   The present invention describes a human aspartyl protease 1 (hu-Aspl)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Gly-Pro. Also described are: (i) a method (II) for assaying hu-Aspl
CC   proteolytic activity, comprising: (a) contacting a hu-Aspl protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Aspl
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the
CC   non-coding strand complementary to a defined 1804 nucleotide sequence
CC   (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC   Aspl proteolytic activity and lacks nucleotides encoding a transmembrane
CC   domain); (3) a purified polynucleotide (III') comprising a sequence that
CC   hybridises under stringent conditions to (III) (the nucleotide sequence
CC   encodes a polypeptide further lacking a pro-peptide domain corresponding
CC   to amino acids 23-62 of hu-Aspl (see ABB78589)); (4) a vector (IV)
CC   comprising (III) or (III'); and (5) a host cell (V) transformed or
CC   transfected with (III), (III') and/or (IV). The hu-Aspl protease
CC   substrate (I) may be used as an enzyme substrate in assays to detect
CC   aspartyl protease activity, (II) and therefore diagnose diseases
CC   associated with aberrant hu-Aspl expression and activity such as
CC   Alzheimer's disease. Hu-Aspl has been localised to chromosome 21, while
CC   hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC   sequence represents human amyloid precursor protein APP695-KK, which is
CC   given in an example from the present invention.
```

```
XX
SQ   Sequence   697 AA;

  Query Match           100.0%;  Score 3651;  DB 23;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 8
AAY88430
ID   AAY88430 standard; Protein; 697 AA.
XX
AC   AAY88430;
XX
DT   03-AUG-2000  (first entry)
XX
DE   Human APP695-VF-KK amino acid sequence.
XX
KW   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW   Alzheimer's disease; beta secretase site; APP695-VF-KK.
XX
OS   Homo sapiens.
XX
PN   WO200017369-A2.
XX
PD   30-MAR-2000.
XX
PF   23-SEP-1999;   99WO-US20881.
XX
PR   24-SEP-1998;   98US-0101594.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2000-303209/26.
DR   N-PSDB; AAA15667.
XX
PT   New enzyme designated human aspartase useful in research into
PT   Alzheimer's Disease is capable of cleaving amyloid protein precursor at
PT   the beta secretase site to produce amyloid beta peptide
XX
PS   Claim 133; Page 148-153; 183pp; English.
XX
CC   This sequence represents a modified version of the human amyloid
CC   precursor protein (APP) amino acid sequence. The sequence is used in an
CC   example of the method of the invention, to show that modification of APP
CC   increases beta amyloid protein processing. The invention relates to a
CC   protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC   amyloid precursor protein (APP). The protease contains a sequence
CC   encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC   separated by 100-300 amino acids. When mutated the APP gene causes an
CC   autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC   surface membrane and have a single C-terminal transmembrane domain.
CC   Proteolytic processing of APP produces the amyloid beta protein, which is
CC   possibly very important in Alzheimer's disease. The invention includes a
CC   nucleotide sequence encoding the protease, a vector containing the
CC   nucleotide sequence, and a cell line comprising the vector. Methods for
CC   screening for inhibitors of beta secretase activity are also given in the
CC   invention. The human aspartase protein and nucleotide sequences and the
CC   methods for identifying inhibitors of the protease, are useful in the
CC   treatment of and research in to Alzheimer's disease.
XX
SQ   Sequence   697 AA;

  Query Match           99.9%;  Score 3646;  DB 21;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 4e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
AAE10637
ID   AAE10637 standard; Protein; 697 AA.
XX
AC   AAE10637;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.
XX
KW   Human; aspartyl protease 1; Aspl; amyloid precursor protein;
KW   Alzheimer's disease; AD; dementia;  neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   APP695-VF-KK; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val substituted with Phe"
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-0023315.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   N-PSDB; AAD17873.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with
PT   amyloid precursor protein processing activity and alpha-secretase
PT   activity, for identifying modulators useful in treating Alzheimer's
PT   disease -
XX
PS   Example 8; Page 120-122; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC   Aspl proteins which lack transmembrane domain or amino terminal
CC   domain or cytoplasmic domain and retains alpha-secretase activity
CC   and amyloid protein precursor (APP) processing activity. The proteins
CC   of the invention are useful for assaying hu-Aspl alpha-secretase
CC   activity, which in turn is useful for identifying modulators of
CC   hu-Aspl alpha-secretase activity, where modulators that increase
CC   hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC   disease (AD) which causes progressive dementia with consequent
CC   formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC   neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC   hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC   the substrate under acidic conditions and determining the level of
CC   hu-Aspl proteolytic activity. The present sequence is human amyloid
CC   protein precursor 695-VF-KK (APP695-VF-KK) isoform. This sequence
CC   is obtained by the addition of two lysine residues (KK motif) at
CC   the C-terminus of App695-VF isoform which is generated by the London
CC   mutation in APP695, where Val at position 642 is replaced with Phe.
CC   APP695-VF-KK isoform is useful for assaying the beta-secretase
CC   activity of human aspartyl protease 2a (hu-Asp2a) protein.
XX
SQ   Sequence   697 AA;

  Query Match             99.9%;  Score 3646;  DB 22;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 4e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTISIATTTTTTTESVEEVVRVPITAASIPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASIPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVFSLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 10
AAE06867
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```
ID   AAE06867 standard; Protein; 697 AA.
XX
AC   AAE06867;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.
XX
KW   Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-VF-KK;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; gene therapy; APP695-VF-KK; mutant;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild type Val substituted with Phe"
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00799.
XX
PR   09-MAY-2001; 2001WO-IB00799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-483072/52.
DR   N-PSDB; AAD13029.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 8; Page 150-152; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting
CC   Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC   blots. The present sequence is modified human amyloid precursor
CC   protein 695-VF-KK (APP695-VF-KK) isoform. APP695-VF-KK isoform is
CC   obtained by addition of two Lys residues (KK motif) at the C-terminal
CC   end of APP695-VF isoform. APP695-VF isoform is obtained by London V-F
CC   mutation in APP695 isoform, where Val at position 642 is replaced with
CC   Phe. APP695-VF-KK isoform is useful for assaying the beta-secretase
CC   activity of human aspartyl protease 2a (Hu-Asp2a) protein.
XX
SQ   Sequence   697 AA;

  Query Match           99.9%;  Score 3646;  DB 22;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 4e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVIPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 11
AAU06611
ID   AAU06611 standard; Protein; 697 AA.
XX
AC   AAU06611;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-VF-KK.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-VF-KK; London mutant; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val substituted by Phe"
FT   Misc-difference 696..697
FT                   /note= "2 Extra Lys residues added compared to
```

FT Wild-type APP695"
XX
PN WO200149098-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00798.
XX
PR 09-MAY-2001; 2001WO-IB00798.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502549/55.
DR N-PSDB; AAS11525.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Example 8; Page 150-152; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridise to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is the human
CC APP695 mutant, APP695-VF-KK which has 2 extra Lys residues added at the
CC C-termunis compared to APP695-VF (the London mutation). The mutation
CC alters the specificity of the APP gamma-secretase activity and increases
CC the rate of processing of the amyloid Abeta peptide.
XX
SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 22; Length 697;
Best Local Similarity 99.9%; Pred. No. 4e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTITTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

RESULT 12
AAU07210
ID AAU07210 standard; Protein; 697 AA.
XX
AC AAU07210;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human beta-amyloid protein precursor, APP695-VF-KK.
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; APP695-VF-KK.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 642
FT /note= "Wild type Val substituted by Phe"
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00797.
XX
PR 09-MAY-2001; 2001WO-IB00797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

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XX
DR   WPI; 2001-502548/55.
DR   N-PSDB; AAS11710.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 8; Page 150-152; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing
CC   an APP cleavage site recognisable by a mammalian beta-secretase, and
CC   further comprising two lysine residues at the carboxyl terminus of the
CC   amino acid sequence of the mammalian APP or APP fragment. The
CC   polypeptides are used for assaying for modulators of beta-secretase
CC   activity; identifying agents that inhibit the APP processing activity
CC   of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC   modulate the activity of Asp2; and for reducing cellular production of
CC   amyloid beta (Abeta) from APP. Agents identified by the above methods
CC   are useful for treating Alzheimer's disease; and for identifying
CC   modulators of amyloid-beta (Abeta) peptide production, for use in
CC   designing therapeutics for the treatment or prevention of Alzheimer's
CC   disease. Probes and primers derived from Asp nucleic acid sequences
CC   are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence represents the
CC   amino acid sequence of human amyloid protein precursor, APP695-VF-KK,
CC   used in the method of the invention.
XX
SQ   Sequence   697 AA;

  Query Match             99.9%;  Score 3646;  DB 22;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 4e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 13
AAE02589
ID   AAE02589 standard; Protein; 697 AA.
XX
AC   AAE02589;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).
XX
KW   Human; alpha-secretase; therapy; amyloid precursor protein 695-VF-KK;
KW   APP695-VF-KK; Alzheimer's disease; antialzheimer's.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26080.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   N-PSDB; AAD06747.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Example 8; Page 149-151; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human APP695-VF-KK. This
CC   sequence is characterised by a V to F alteration at position 642
CC   and contains two carboxy-terminal lysine residues.
XX
SQ   Sequence   697 AA;

  Query Match             99.9%;  Score 3646;  DB 22;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 4e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTIESVEEVVRVPTTAASTPDAV 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 14
ABB78598
ID   ABB78598 standard; Protein; 697 AA.
XX
AC   ABB78598;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human APP695-VF-KK protein sequence SEQ ID NO:20.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW   proteolytic; amyloid precursor protein; APP.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-0025934.
XX
PR   23-SEP-1999;   99US-155493P.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-169232P.
PR   22-SEP-2000; 2000GB-0023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M.
XX
DR   WPI; 2002-396337/43.
DR   N-PSDB; ABL52465.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect
PT   aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PI   disease -
XX
PS   Example 8; Page 120-122; 182pp; English.
XX
CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Glu-Pro. Also described are: (1) a method (II) for assaying hu-Aspl
CC   proteolytic activity, comprising: (a) contacting a hu-Aspl protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Aspl
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the
CC   non-coding strand complementary to a defined 1804 nucleotide sequence
CC   (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC   Aspl proteolytic activity and lacks nucleotides encoding a transmembrane
CC   domain); (3) a purified polynucleotide (III') comprising a sequence that
CC   hybridises under stringent conditions to (III) (the nucleotide sequence
CC   encodes a polypeptide further lacking a pro-peptide domain corresponding
CC   to amino acids 23-62 of hu-Aspl (see ABB78589)); (4) a vector (IV)
CC   comprising (III) or (III'); and (5) a host cell (V) transformed or
CC   transfected with (III), (III') and/or (IV). The hu-Aspl protease
CC   substrate (I) may be used as an enzyme substrate in assays to detect
CC   aspartyl protease activity, (II) and therefore diagnose diseases
CC   associated with aberrant hu-Aspl expression and activity such as
CC   Alzheimer's disease. Hu-Aspl has been localised to chromosome 21, while
CC   hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC   sequence represents human amyloid precursor protein APP695-VF-KK, which
CC   is given in an example from the present invention.
XX
SQ   Sequence   697 AA;

  Query Match             99.9%;  Score 3646;  DB 23;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 4e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 15
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ID   AAY88429 standard; Protein; 697 AA.
XX
AC   AAY88429;
XX
DT   03-AUG-2000  (first entry)
XX
DE   Human APPSW-KK amino acid sequence.
XX
KW   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW   Alzheimer's disease; beta secretase site; APPSW-KK.
XX
OS   Homo sapiens.
XX
PN   WO200017369-A2.
XX
PD   30-MAR-2000.
XX
PF   23-SEP-1999;   99WO-US20881.
XX
PR   24-SEP-1998;   98US-0101594.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2000-303209/26.
DR   N-PSDB; AAA15666.
XX
PT   New enzyme designated human aspartase useful in research into
PT   Alzheimer's Disease is capable of cleaving amyloid protein precursor at
PT   the beta secretase site to produce amyloid beta peptide
XX
PS   Claim 133; Page 143-147; 183pp; English.
XX
CC   This sequence represents a modified version of the human amyloid
CC   precursor protein (APP) amino acid sequence. The sequence is used in an
CC   example of the method of the invention, to show that modification of APP
CC   increases beta amyloid protein processing. The invention relates to a
CC   protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC   amyloid precursor protein (APP). The protease contains a sequence
CC   encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC   separated by 100-300 amino acids. When mutated the APP gene causes an
CC   autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC   surface membrane and have a single C-terminal transmembrane domain.
CC   Proteolytic processing of APP produces the amyloid beta protein, which is
CC   possibly very important in Alzheimer's disease. The invention includes a
CC   nucleotide sequence encoding the protease, a vector containing the
CC   nucleotide sequence, and a cell line comprising the vector. Methods for
CC   screening for inhibitors of beta secretase activity are also given in the
CC   invention. The human aspartase protein and nucleotide sequences and the
CC   methods for identifying inhibitors of the protease, are useful in the
CC   treatment of and research in to Alzheimer's disease.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3643;  DB 21;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 6.6e-256;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 14:00:39 ; Search time 39 Seconds
(without alignments)
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Title: US-09-806-194-16
Perfect score: 3651
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Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3651	100.0	697	9	US-09-795-847-16	Sequence 16, Appl
3	3651	100.0	697	9	US-09-794-743-16	Sequence 16, Appl
4	3651	100.0	697	9	US-09-794-748-16	Sequence 16, Appl
5	3651	100.0	697	9	US-09-794-925-16	Sequence 16, Appl
6	3651	100.0	697	9	US-09-681-442-16	Sequence 16, Appl
7	3651	100.0	697	11	US-09-869-414-16	Sequence 16, Appl
8	3651	100.0	697	11	US-09-548-366-16	Sequence 16, Appl
9	3646	99.9	697	9	US-09-794-927-20	Sequence 20, Appl
10	3646	99.9	697	9	US-09-795-847-20	Sequence 20, Appl
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13	3646	99.9	697	9	US-09-794-925-20	Sequence 20, Appl
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16	3646	99.9	697	11	US-09-548-366-20	Sequence 20, Appl
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21	3643	99.8	697	9	US-09-794-925-18	Sequence 18, Appl
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ALIGNMENTS

RESULT 1
US-09-794-927-16
; Sequence 16, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
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Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 2
US-09-795-847-16
; Sequence 16, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 3
US-09-794-743-16
; Sequence 16, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang

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;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-794-748-16

  Query Match           100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-225;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 4
US-09-794-748-16
; Sequence 16, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-794-748-16

  Query Match           100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-225;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 5
US-09-794-925-16
; Sequence 16, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 6
US-09-681-442-16
; Sequence 16, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 7
US-09-869-414-16
; Sequence 16, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-869-414-16

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  Query Match           100.0%;  Score 3651;  DB 11;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-225;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 8
US-09-548-366-16
; Sequence 16, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881

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;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-366-16

  Query Match           100.0%;  Score 3651;  DB 11;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-225;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
US-09-794-927-20
; Sequence 20, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michae. J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
;  TITLE OF INVENTION:  CSES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280PS
;  CURRENT APPLICATION NUMBER: US/09/794,927
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,233
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-927-20

  Query Match           99.9%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 2.2e-225;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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RESULT 10
US-09-795-847-20
; Sequence 20, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-795-847-20

  Query Match           99.9%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 2.2e-225;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 11
US-09-794-743-20
; Sequence 20, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-794-743-20

  Query Match           99.9%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 2.2e-225;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 12
US-09-794-748-20
; Sequence 20, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-20

Query Match 99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVIPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 13
US-09-794-925-20
; Sequence 20, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-20

Query Match 99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 14
US-09-681-442-20
; Sequence 20, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-20

Query Match 99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 15
US-09-869-414-20
; Sequence 20, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-869-414-20

  Query Match             99.9%;  Score 3646;  DB 11;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 2.2e-225;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHILKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


Search completed: October  2, 2003, 14:18:35
Job time : 41 secs
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:04 ; Search time 16.6667 Seconds
(without alignments)
4021.774 Million cell updates/sec

Title: US-09-806-194-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3641	99.7	695	1	A49795	Alzheimer's diseas
2	3590.5	98.3	770	1	QRHUA4	Alzheimer's diseas
3	3544	97.1	695	2	S00550	Alzheimer's diseas
4	3519	96.4	695	2	A27485	Alzheimer's diseas
5	3103	85.0	747	2	JH0773	Alzheimer's diseas
6	2105	57.7	484	4	A32761	hypothetical Alzhe
7	1728	47.3	763	2	A49321	amyloid beta (A4)
8	1716	47.0	765	2	S42880	amyloid precursor-
9	1704	46.7	751	2	A49974	beta-amyloid precu
10	1185	32.5	653	2	A46362	amyloid precursor-
11	1143	31.3	511	2	JC1404	CDEI-box DNA-bindi
12	817.5	22.4	686	2	T15795	hypothetical prote
13	747	20.5	886	2	A32758	beta-amyloid-like
14	706	19.3	246	2	S38344	CDEI-binding prote
15	411	11.3	82	2	PQ0438	Alzheimer's diseas
16	296.5	8.1	191	2	A35981	sperm membrane pro
17	283	7.8	57	2	E60045	Alzheimer's diseas
18	283	7.8	57	2	F60045	Alzheimer's diseas
19	283	7.8	57	2	G60045	Alzheimer's diseas
20	283	7.8	57	2	D60045	Alzheimer's diseas
21	283	7.8	57	2	A60045	Alzheimer's diseas
22	283	7.8	57	2	B60045	Alzheimer's diseas
23	217	5.9	42	2	PN0512	beta-amyloid prote
24	192.5	5.3	1110	2	I51116	NF-180 - sea lampr
25	186	5.1	5170	2	T15348	hypothetical prote
26	185.5	5.1	407	1	EDBEQ3	immediate-early pr
27	185.5	5.1	993	2	S49461	synaptonemal compl
28	182	5.0	522	2	T32444	hypothetical prote
29	175.5	4.8	802	1	S48529	NAB3 protein - yea
30	175.5	4.8	1188	2	T46608	zinc finger protei
31	174.5	4.8	464	2	H90279	microtubule bindin
32	174.5	4.8	884	2	T20405	hypothetical prote
33	174	4.8	579	2	JH0820	160K golgi antigen
34	174	4.8	1087	2	T30330	gelsolin-related p
35	173.5	4.8	793	1	JH0628	caldesmon - human
36	172	4.7	771	1	A33430	h-caldesmon - chic
37	172	4.7	784	2	PN0009	neurofilament trip
38	172	4.7	1182	2	T30189	myelin transcripti
39	171	4.7	1271	2	A45555	glutamate rich pro
40	170	4.7	1948	2	S00485	gene 11-1 protein
41	169.5	4.6	298	1	TPHUTC	troponin T, cardia
42	169.5	4.6	721	2	S29795	hypothetical prote
43	169	4.6	885	2	G71608	ATP-dept. acyl-CoA
44	169	4.6	1187	2	T46637	transcription fact
45	168.5	4.6	675	2	T03744	myoD protein inhib

ALIGNMENTS

RESULT 1
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human suppo
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote
C;Keywords: alternative splicing

Query Match 99.7%; Score 3641; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 2
QRHUA4
Alzheimer's disease amyloid beta protein precursor (validated) - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A4
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-protd
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral h
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Al
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; And
erakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; M
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds fo
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik,
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovasc
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
```

A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30059.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for resi
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for res
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreutl

Query Match 98.3%; Score 3590.5; DB 1; Length 770;
Best Local Similarity 90.1%; Pred. No. 2e-181;
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGIK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                  :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANIENEVEPVDARPAADRGLTTRPGSGLTN 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
```

RESULT 3
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg,
EMBO J. 7, 1365-1370, 1988

```
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brai
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

  Query Match             97.1%;  Score 3544;  DB 2;  Length 695;
  Best Local Similarity   97.3%;  Pred. No. 5e-179;
  Matches  676;  Conservative    7;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| |||||||||||||||:|||||:||:|||||||.|||:'||||;
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||| ||||||||||||||||||||:||||| | ||.|||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||:|||| |||||||||||||||| ||||||||||||||:|||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||::||| |||||||||||||.|||||| |||||||||||'|||:| ||
Db        181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||:||| ||||||||||.|||||||||||||.|||||.|||||||||.|||:|||
Db        241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              |||||||||||||||||.|||||||||||||||:|||||| |||||||||:|||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              |||||||||||||||||.|||||||||||||||||||||'|||||'|| ||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              :||||:|||||||||||||||||||||:|||||||||||||| ||||||:|||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||:||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||:|| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||'|||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 4
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzhe
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C;Keywords: alternative splicing; amyloid; transmembrane protein

  Query Match             96.4%;  Score 3519;  DB 2;  Length 695;
  Best Local Similarity   96.8%;  Pred. No. 1e-177;
  Matches  673;  Conservative    5;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| |||||||||||||||||||||||||:|||||||||||:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||'|||||||||||||||||||||||||||||||||||||| | |||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||:||||||||||||| |||||||| |||||||||||||||:||||
Db        181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWVGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLDLENYITALQAVPPRPRHVFNMLKK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKATQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLITRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match            85.0%;  Score 3103;  DB 2;  Length 747;
  Best Local Similarity  81.0%;  Pred. No. 8.3e-156;
  Matches  598;  Conservative   35;  Mismatches   41;  Indels   64;  Gaps    5;

Qy         17 ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQE 75

Db         15 ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE 71

Qy         76 VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF 135

Db         72 VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF 131

Qy        136 LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN 195

Db        132 LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEESES 191

Qy        196 VDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDEDDEDGDE 253

Db        192 FDSADAAEDDCDVWWGGADADYVDRSDDKAVEAQPDEEEEVVEVEEEETDDDED--DGDE 249

Qy        254 VEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------------------------- 288

Db        250 AEEEPEEPYEEAIERTTSIATTTTTTIESVEEVVREVCSEQAETGPCRAMISRWYYDVTE 309

Qy        289 ------------------------------VPTIAASTPDAVDKYLETPGDENEHAHFQ 317

Db        310 SKCAQFIYGGCGGNRNNFESDDYCMAVCGSVIPATAASTPDAVDKYLENPNDENEHDRFL 369

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQ 377

Db        370 KAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ 429

Qy        378 LVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 437

Db        430 LVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 489

Qy        438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNY 497

Db        490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAVAEEIQDEVDELFQKEQNY 549

Qy        498 SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAN 557

Db        550 SDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPWHSFGVDSVPAN 609

Qy        558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA 617

Db        610 TENEVEPVDARPAADRGLTIRPGSGLTNIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669

Qy        618 EDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKM 677

Db        670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTIIHHGVVEVDAAVIPEERHLTKM 729

Qy        678 QQNGYENPTYKFFEQMQN 695

Db        730 QQNGYENPTYKFFEQMQN 747


RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - huma
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C;Accession: A32761
R;de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A;Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secr
A;Reference number: A32761; MUID:89346754; PMID:2569763
A;Accession: A32761
A;Molecule type: mRNA
A;Residues: 1-484 <DES>
A;Cross-references: GB:M28373
A;Note: the authors translated the codon ATG for residue 433 as Leu
C;Comment: This is the hypothetical translation of a sequence believed to contain
C;Keywords: cloning artifact

  Query Match            57.7%;  Score 2105;  DB 4;  Length 484;
  Best Local Similarity  87.7%;  Pred. No. 1.4e-103;
  Matches  407;  Conservative    1;  Mismatches    0;  Indels   56;  Gaps    1;

Qy         80 LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQE 139

Db          1 LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQE 60

Qy        140 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 199

Db         61 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 120

Qy        200 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAE 259

Db        121 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAE 180

Qy        260 EPYEEATERTTSIATTTTTTTESVEEVVR---------------------------- 288

Db        181 EPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPF 240
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Qy        289 ------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 323
                                      :|||||.|||||||||:|||||.|||: |||||
Db        241 PYGGCGGNRNNFDTEEYCMAVCGSAIPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 300

Qy        324 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM 383
              |||||||||||||||||.|||||||||||||||||||||||||||||||||||||||||!
Db        301 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM 360

Qy        384 ARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 443
              |||||||||:|||||||||||:|||||||||||:|||||||||||||||||||||||||`
Db        361 ARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 420

Qy        444 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV 487
              |||||||||||||| ||||| |||||||||| |||||'|||||.|
Db        421 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV 464


RESULT 7
A49321
amyloid beta (A4) homolog 2 precursor - human
N;Alternate names: CDEI-binding protein
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49321; S34644; S40519
R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
A;Reference number: A49321; MUID:93250009; PMID:8485127
A;Accession: A49321
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <SPR>
A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60569.1; PID:g300169
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)
A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A;Description: The human homologue of the murine CDEI binding protein is an amyloid prec
A;Reference number: S34644
A;Accession: S34644
A;Molecule type: mRNA
A;Residues: 1-763 <VON>
A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A;Reference number: S40519; MUID:94035131; PMID:8220435
A;Accession: S40519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <WAS>
A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C;Genetics:
A;Gene: GDB:APLP2; APPL2
A;Cross-references: GDB:139159; OMIM:104776
A;Map position: 11q23-11q25
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; transmembrane protein
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             47.3%;  Score 1728;  DB 2;  Length 763;
  Best Local Similarity   47.1%;  Pred. No. 1.7e-83;
  Matches  372;  Conservative  112;  Mismatches  165;  Indels  140;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | ||||   || || :         |||    :|||||||||:|||:|:| ||| :||
Db         15 LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:| :||| :|||||||:|||||||:|:|||. |:| :||:| :|||:   |' :::
Db         75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||||||||: |||||:||:| |:|||:||| | |||:| || | :   |: |||||||:
Db        133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMILYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|||| :  :|  : |||:       : :  |  || |  :|   |:
Db        193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-------EEEEEDEEEDYDVYKSEPPTEAD 245

Qy        237 VEE--EEA--DDDEDDEDGDEVEEEAEEPY----------EEATERTTSIATTTTTTTES 282
              :|:  | |  :||||:|:|:|| |: :  |          |  ||  :    :   |
Db        246 LEDFTEAAVDEDDEDEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy        283 VEEV-------------------------------------------------VRVP 290
              ': |                                                 :|
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMIP 365

Qy        291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPK 350
              |   | | || | ||  |:|||| :||||:|| :|| || :: :|||||| ||||||
Db        366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy        351 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPP 410
              |::: :|||||  |::|:|:|||:|:|||||||:|||||||||||:|:|||||: ||| ||
Db        425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP 484

Qy        411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 470
              ||  :   |::|||| :|| |:::|::|| |||:||||::|||||| '| || ||||
Db        485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSL 544

Qy        471 SLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVE 530
              |||| || ||:|||:':|||||.:::      |:|      '    |:|||   |
Db        545 SLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTASISEIPVDVR 587

Qy        531 LLPVNGEFSLDDLQPWHSFGADSVPANIENEVEPVDARPAADRGLTTRPGSGLTN----- 585
                : | | ::: |:| |     || |||    | :|     :  : |||:
Db        588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGGL 635

Qy        586 IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKG 625
              |  ||    |: |:|     '   :|  ::::| ||:||                 :
Db        636 IGAEEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEEERESVGPLREDFSLSSS 693

Qy        626 AIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENP 685
              |:|||:|  | |||||||:||||:|:|| :| ||:|||  :|||||||:||| :|||||
Db        694 ALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENP 753

Qy        686 TYKFFEQMQ 694
              |||: ||||
Db        754 TYKYLEQMQ 762


RESULT 8
S42880
amyloid precursor-like protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S42880; S47528
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A;Description: Complete nucloetide ad deduced amino acid sequence of rat amyloid p
A;Reference number: S42880
A;Accession: S42880
A;Molecule type: mRNA
A;Residues: 1-765 <SAN>
A;Cross-references: EMBL:X77934
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein
A;Reference number: S47528; MUID:94368849; PMID:8086458
A;Accession: S47528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-765 <SA2>
A;Cross-references: EMBL:X77934
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
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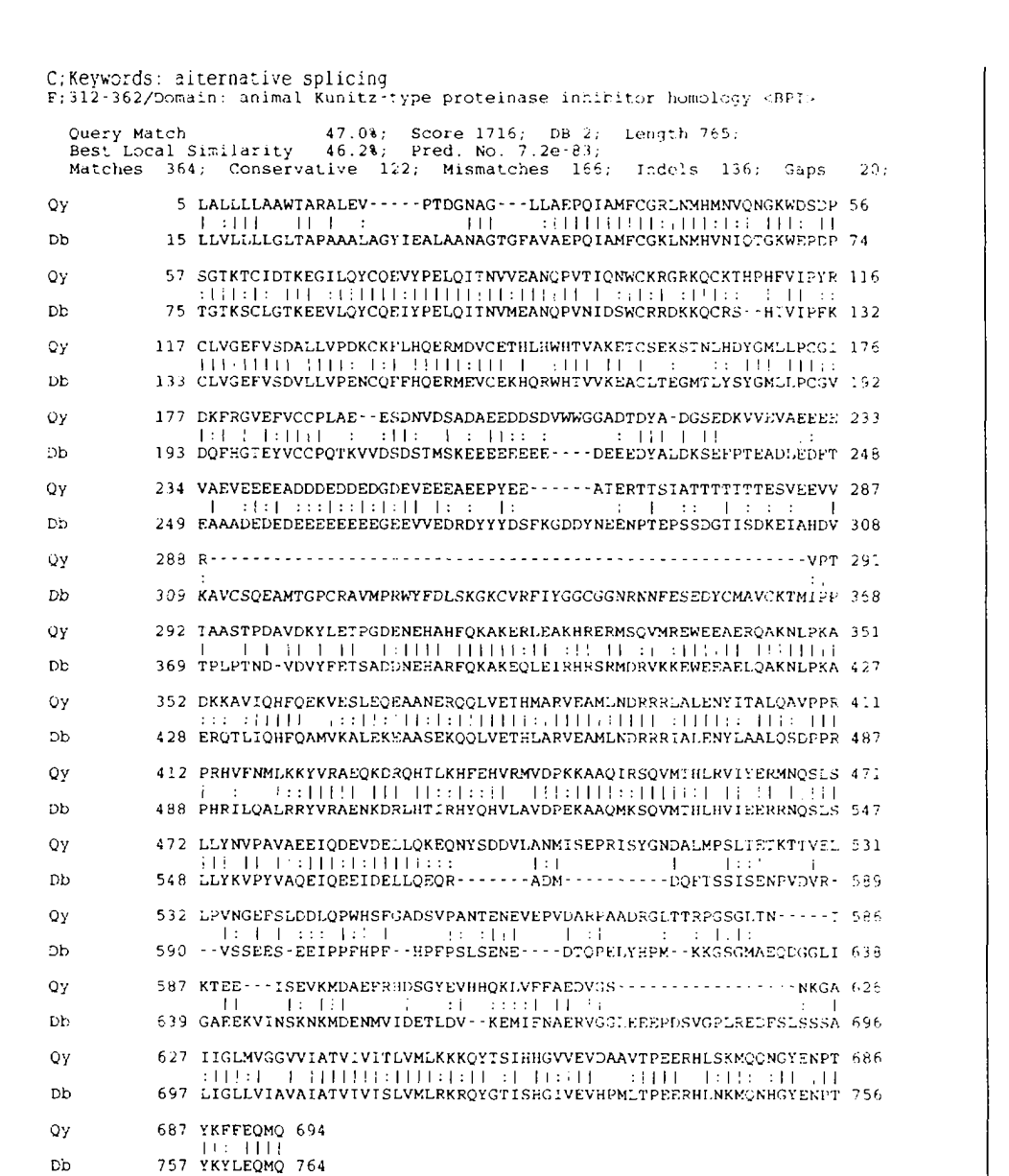
C;Keywords: alternative splicing
F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

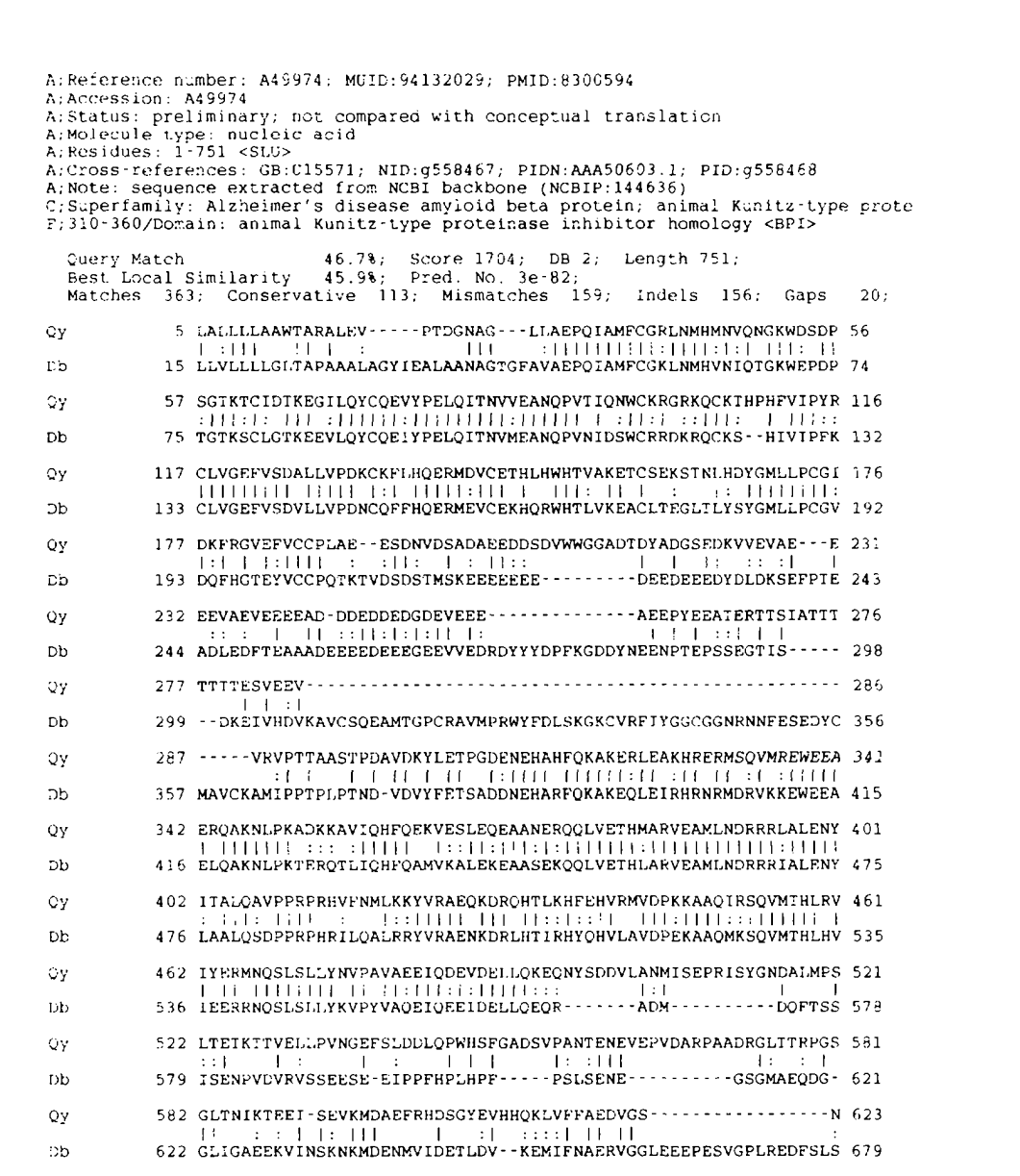
Query Match 47.0%; Score 1716; DB 2; Length 765;
Best Local Similarity 46.2%; Pred. No. 7.2e-83;
Matches 364; Conservative 122; Mismatches 166; Indels 136; Gaps 20;



RESULT 9
A49974
beta-amyloid precursor protein 2 homolog APLP2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49974
R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid

A;Reference number: A49974; MUID:94132029; PMID:8300594
A;Accession: A49974
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-751 <SLU>
A;Cross-references: GB:C15571; NID:g558467; PIDN:AAA50603.1; PID:g558468
A;Note: sequence extracted from NCBI backbone (NCBIP:144636)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.7%; Score 1704; DB 2; Length 751;
Best Local Similarity 45.9%; Pred. No. 3e-82;
Matches 363; Conservative 113; Mismatches 159; Indels 156; Gaps 20;



RESULT 10
A46362

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amyloid precursor-like protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A46362
R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
A;Title: Identification of a mouse brain cDNA that encodes a protein related to the Alzh
A;Reference number: A46362; MUID:93066322; PMID:1279693
A;Accession: A46362
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-653 <WAS>
A;Experimental source: brain
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: transmembrane protein

  Query Match            32.5%;  Score 1185;  DB 2;  Length 653;
  Best Local Similarity   38.6%;  Pred. No. 4.9e-55;
  Matches  270;  Conservative  121;  Mismatches  231;  Indels   78;  Gaps   17;

Qy          1 MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGT 59
Db         22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy         60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
Db         81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAIPMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy        119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
Db        141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDR 200

Qy        179 FRGVEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
Db        201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-------EEEVESP 248

Qy        238 EEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
Db        249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR--------PT------ 294

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
Db        295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
Db        355 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
Db        415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
Db        475 HLAQELRPQIQELL----------LAEHLGPSEL----DASVPGSSSEDK---------- 510

Qy        537 EFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
Db        511 ----GSLQP-----------PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYEQ 551

Qy        597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML-KKKQ 652
Db        552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSLIVLSLLLLRKKKP 611

Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
Db        612 YGTISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 651

RESULT 11
JC1404
```

```
CDEI-box DNA-binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C;Accession: JC1404
R;Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
A;Title: A murine sequence-specific DNA binding protein shows extensive local simi
A;Reference number: JC1404; MUID:93129193; PMID:1482349
A;Accession: JC1404
A;Molecule type: mRNA
A;Residues: 1-511 <VID>
C;Comment: This protein plays an important role in the early development of the mo
C;Keywords: DNA binding; transmembrane protein

  Query Match            31.3%;  Score 1143;  DB 2;  Length 511;
  Best Local Similarity   45.8%;  Pred. No. 5.8e-53;
  Matches  253;  Conservative   92;  Mismatches  128;  Indels   80;  Gaps   16;

Qy        174 CGIDKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE- 230
Db          6 CGVDQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEF 56

Qy        231 --EEEVAEVEEEEAD-DDEDDEDGDEVEEEAE--------EPYEEATERTTSIATTTTTI 279
Db         57 PTEADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTIS 114

Qy        280 TESVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWE 339
Db        115 DKEIVHDVKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWE 173

Qy        340 EAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALE 399
Db        174 EAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALE 233

Qy        400 NYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHL 459
Db        234 NYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHL 293

Qy        460 RVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALM 519
Db        294 HVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFT 336

Qy        520 PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRP 579
Db        337 SSISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE---------GSGMAEQD 380

Qy        580 GSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS--------------- 622
Db        381 G-GLIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFS 437

Qy        623 -NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNG 681
Db        438 LSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHG 497

Qy        682 YENPTYKFFEQMQ 694
Db        498 YENPTYKYLEQMQ 510

RESULT 12
T15795
hypothetical protein C42D8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C;Accession: T15795; A49414
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C42D8.
A;Reference number: Z18405
A;Accession: T15795
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-686 <HAL>
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A;Cross-references: EMBL:U56966; NID:g1293844; PID:g1293850; PIDN:AAA98722.1; GSPDB:GN0
A;Experimental source: strain Bristol N2; clone C42D8
R;Daigle, I.; Li, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993
A;Title: apl-1, a Caenorhabditis elegans gene encoding a protein related to the human be
A;Reference number: A49414; MUID:94089766; PMID:8265668
A;Accession: A49414
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-686 <DAI>
A;Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297
C;Genetics:
A;Gene: CESP:C42D8.8
A;Map position: X
A;Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 583/3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

  Query Match             22.4%;  Score 817.5;  DB 2;  Length 686;
  Best Local Similarity   29.1%;  Pred. No. 1.1e-35;
  Matches  222;  Conservative  110;  Mismatches  275;  Indels  155;  Gaps   22;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGIK 60
              :: || : :| | ' |   |         . :|  ;|  | :|  :   | :|
Db          6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||   |  ,|:||:: || : |||:|) :  ):| :|||:      ||    ) | || ): |
Db         64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN------LHDYGMLLPC 174
              || |:|| ||  |:| |    | |  : ||   | : |  | :         :  : :, ||
Db        123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy        175 GIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV 234
              :| | ||||||||    :|  :  | ::
Db        183 ALDMFTGVEFVCCP----NDQTNKTDVQKTK------------------------------ 209

Qy        235 AEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAA 294
                |:|: ||||||    |:   |::|  ||
Db        210 ---EDEDDDDDEDDAYEDDYSEESDEKDEE------------------------------ 236

Qy        295 STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA-----ERQAKNLP 349
              | : | |  :     |||  |:||: |:: || ::: :|':|| :      |::||: :
Db        237 -EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHRKKVDKVMKEWGDLETRYNEQKAKD-P 294

Qy        350 KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL- 405
              |  :|   !    ||: | |||:|    |:::    ,  ||:| ||:::  |  :|  ||
Db        295 KGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA 354

Qy        406 -QAVPPRPRHVFNMLKKYVRAEQKDRQHILKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE 464
               |    |   || |:|||:|| |||  : |:   | :|,|  :  |:   | |
Db        355 THVNKPNKHSVLQSLKAYIRAEESKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL 414

Qy        465 RMNQSLSLLYNVP---------AVA--EEIQLEVDELLQKEQNYSDDVLANMISEPRISY 513
              |:| :|:|: | |         !!   :: : ||   :  |    |     :|  :   |
Db        415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE----DSELTPIIHDDEFSK 470

Qy        514 GN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANI---ENEVEP 564
                 |   |: |    :      :|!!     | ::   ::     |      |   : :|:
Db        471 NAKLDVKAPTTTAKPVKEIDNAKVLPTEASDSEEEADEYYEDEDDEQVKKIPDMKKKVKV 530

Qy        565 VDARP--------------------AADRGLTTRPGSGLTNIKTEE-----ISEVKMDA 598
              || :|                    |       |  |: :::|      | |::::|
Db        531 VDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSSESDEDEDKNIKELRVDI 590

Qy        599 E---------FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVIILVMLK 649
              |         :|||        ||:   |   |         ::   :  | | |    :
Db        591 EPIIDEPASFYRHD--------KLIQSPEVERSASSVFQPYVLASAMFITAICIIAFAIT 642

Qy        650 KKQYTSIHHGVVEVDAAVIPEERHLSKMQQNGYENPTYKFFE 691
              :    | :||;   |||||:: || |||||||  ||:
Db        643 NARRRRAMRGFIEVD-VYIPEERHVAGMQVNGYENPTYSFFD 683


RESULT 13
A32758
beta-amyloid-like protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 24-Sep-1998
C;Accession: A32758
R;Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989
A;Title: A Drosophila gene encoding a protein resembling the human beta-amyloid p
A;Reference number: A32758; MUID:89184650; PMID:2494667
A;Accession: A32758
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-886 <ROS>
A;Cross-references: GB:J04516; NID:g158371; PID:g158372
C;Genetics:
A;Gene: FlyBase:Appl
A;Cross-references: FlyBase:FBgn0000108
C;Keywords: transmembrane protein

  Query Match             20.5%;  Score 747;  DB 2;  Length 886;
  Best Local Similarity   25.5%;  Pred. No. 7.7e-32;
  Matches  233;  Conservative  127;  Mismatches  288;  Indels  264;  Gaps   29;

Qy          7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDSDPSG 58
              ||| : |   |:      | | : |     |||||: |  |::      : : |:| :| |
Db          9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVTDLSK 63

Qy         59 T---KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
                   ||:  |  :| ||:: ||   |||:|||::    |  ||:::|     :||    ::
Db         64 KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWI 123

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
              |:||| | | |||||||: | | |       |   : |:       | |:   :  : |||
Db        124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRTFAMLL 182

Qy        173 PCGIDKFRGVEFVCCP-----------------------------LAEESDNVD---SA 199
              |||| | ||||||||                             : :| |: |   |
Db        183 PCGISVFSGVEFVCCPKHFKTDEIHVKKTDLPVMPAAQINSANDELMNDEDDSNDSNYSK 242

Qy        200 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV----------------------AEV 237
              || ||| |       | |   | :::   ||:|                         ||
Db        243 DANEDDLD------DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINAEY 296

Qy        238 EE-EEADDDEDDEDGDEVEEEAEEPY--------------------------EEATERT 269
              :  || |: ::|  | | | | | :                          |:|  ::
Db        297 DSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLKSDSSSPSSAPVAPAPEKAPVKS 356

Qy        270 TSIATTTTTTTESVEEVV----------RVPTTAASTPDAVDKYLETPGDENEHAHFQK 318
              |: :|   :  :  |               |:|| :    | |          ||  ::
Db        357 ESVTSTPQLSASAAAPVAANSGNSGTGAGAPPSTAQPTS---DPYFTHFDPHYEHQSYKV 413

Qy        319 AKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKA-------VIQHFQEKVESLEQEA 371
              :::|||  |||:::::|:::| : | : :::  || ||       :   ||  |::||:|
Db        414 SQKRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFKQRMTARFQTSVQALEEEG 473

Qy        372 ANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQ 431
              |: ||   |  || | :| |:| |:  |  ||   ||   ||   |:| |:|  :||  |||
Db        474 NAEKHQLAAMHQQRVLAHINQRKREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDRA 533

Qy        432 HTLKHFEH-VRMVDP---KKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI---- 483
              | | |: : :    |  : || |  : :  |  |   :|||:::|   | :: :|
Db        534 HALAHYRHLLNSGGPGGLEAAASERPRTLERLIDIDRAVNQSMTMLKRYPELSAKIAQLM 593

Qy        484 ---------QDEV---------------------------------------------- 487
                      :|::
Db        594 NDYILALRSKDDIPGSSLGMSEEAEAGILDKYRVEIERKVAEKERLRLAEKQRKEQRAAE 653

Qy        488 -----DELLQKEQNYSDDVLANMISE----------------------PRISYGNDALM 519
                  :| |: |    ||:| : ::|                        |    | || :
Db        654 REKLREEKLRLEAKKVDDMLKSQVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAAL 713
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Qy        520 -----PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRG 574
                   |:|  ||:        |  | | :    :|  :'       |      |  |
Db        714 VTAANPNLETTKS---------EKDLSDTE----YGEATVSTTKVQTVLPTVDDDAVQRA 760

Qy        575 LTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---GA 626
              :     :         ::  : : : :|   ::: |:: |     ||:   : |
Db        761 VEDVAAA---------VAHQEAEPQVQHFMTHDLGHRESFSLRREFAQHAHAAKEGRNV 811

Qy        627 IIGLMVGGVVIATVIVITLVMLKKKQYTSIH-HGVVEVDAAVTP------EERHLSKMQQ 679
                |   |: :   : : : : | :   | :  | :||:  ||       ||: :  ||
Db        812 YFTLSFAGIALMAAVFVGVAVAKWRTSRSPHAQGFIEVDQNVITHHPIVREEKIVPNMQI 871

Qy        680 NGYENPTYKFFE 691
              ||||||||||:||
Db        872 NGYENPTYKYFE 883


RESULT 14
S38344
CDEI-binding protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May 1996
C;Accession: S38344
R;Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.
Biochim. Biophys. Acta 1216, 154-156, 1993
A;Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
A;Reference number: S38344; MUID:94032480; PMID:8218408
A;Accession: S38344
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-246 <HAN>
A;Cross-references: EMBL:Z22592
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

  Query Match             19.3%;  Score 706;  DB 2;  Length 246;
  Best Local Similarity   51.5%;  Pred. No. 2.2e-30;
  Matches  136;  Conservative   35;  Mismatches   51;  Indels   42;  Gaps    7;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              ! :|||   || :  :         |||    :|||.:'| |||:|||:.:| :' : |
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGPAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|:|:|: |:| :|||||:|:||||||||||:|.|||' ; :|||, :::|.:    |||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||:|||| |||| |:| |||||:||| :  |||: || |  :   :: ||||||||:
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|||   ::  |||                    |  :   ! ||
Db        193 DQFHGTEYVCCP---QTKTVDS----------------------DSIMSKEEEEE--- 222

Qy        237 VEEEEADDDED-DEDGDEVEEEAE 259
               ||:| |::|| ! | |  ||:
Db        223 -EEDEEDEEEDYDLDKSEFPTEAD 245


RESULT 15
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide i
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

  Query Match             11.3%;  Score 411;  DB 2;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-15;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        581 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATV 640
              ||||||||||:||||||||||||||||||||||||||:|||||||||||||||||||||||
Db          1 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATV 60

Qy        641 IVITLVMLKKKQYTSIHHGVVE 662
              ||||||||||:||||||||||:
Db         61 IVITLVMLKKKQYTSIHHGVVE 82


Search completed: October 2, 2003, 14:00:31
Job time : 20.6667 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:24 ; Search time 10 Seconds
(without alignments)
3277.761 Million cell updates/sec

Title: US-09-806-194-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3590.5	98.3	770	1	A4_HUMAN	P05067 h amyloid b
2	3590.5	98.3	770	1	A4_MACFA	P53601 m amyloid b
3	3584	98.2	751	1	A4_SAISC	Q95241 s amyloid b
4	3535.5	96.8	770	1	A4_PIG	P79307 s amyloid b
5	3522.5	96.5	770	1	A4_CAVPO	Q60495 c amyloid b
6	3493.5	95.7	770	1	A4_MOUSE	P12023 m amyloid b
7	3493.5	95.7	770	1	A4_RAT	P08592 r amyloid b
8	1735	47.5	695	1	APP2_MOUSE	Q06335 mus musculu
9	1728	47.3	763	1	APP2_HUMAN	Q06481 homo sapien
10	1716	47.0	765	1	APP2_RAT	P15943 rattus norv
11	1190	32.6	650	1	APP1_HUMAN	P51693 homo sapien
12	1185	32.5	653	1	APP1_MOUSE	Q03157 mus musculu
13	817.5	22.4	686	1	A4_CAEEL	Q10651 caenorhabdi
14	748.5	20.5	887	1	A4_DROME	P14599 drosophila
15	292	8.0	59	1	A4_BOVIN	Q28053 bos taurus
16	288	7.9	58	1	A4_RABIT	Q28748 oryctolagus
17	288	7.9	58	1	A4_SHEEP	Q28757 ovis aries
18	287	7.9	58	1	A4_CANFA	Q28280 canis fami
19	283	7.8	57	1	A4_URSMA	Q29149 ursus marit
20	185.5	5.1	407	1	IE68_HSVSA	Q01042 herpesvirus
21	185.5	5.1	993	1	SCP1_MOUSE	Q62209 mus musculu
22	176	4.8	2004	1	MO2_HUMAN	Q92794 homo sapien
23	175.5	4.8	802	1	NAB3_YEAST	P38996 saccharomyc
24	174	4.8	579	1	G160_HUMAN	Q08378 homo sapien
25	173.5	4.8	793	1	CALD_HUMAN	Q05682 homo sapien
26	172	4.7	771	1	CALD_CHICK	P12957 gallus gall
27	169.5	4.6	297	1	TRT2_HUMAN	P45379 homo sapien
28	169.5	4.6	721	1	YCF2_OENPI	P31568 oenothera p
29	168.5	4.6	1875	1	MLP1_YEAST	Q02455 saccharomyc
30	168	4.6	1240	1	YNJ1_YEAST	P53935 saccharomyc
31	167.5	4.6	1976	1	MYHA_HUMAN	P35580 homo sapien
32	166.5	4.6	1976	1	YG3A_YEAST	P53278 saccharomyc
33	166.5	4.6	1976	1	MYHA_RAT	Q9jlt0 rattus norv
34	164.5	4.5	1325	1	G160_MOUSE	P55937 mus musculu
35	163.5	4.5	681	1	MP10_HUMAN	O00566 homo sapien
36	163	4.5	2017	1	MYSN_DROME	Q99323 drosophila
37	162.5	4.5	712	1	NUCL_RAT	P13383 rattus norv
38	160.5	4.4	1976	1	MYHA_BOVIN	Q27991 bos taurus
39	160	4.4	694	1	NUCL_CHICK	P15771 gallus gall
40	159.5	4.4	1955	1	PUMA_PARUN	O61308 parascaris
41	158	4.3	301	1	TRT2_CHICK	P02642 gallus gall
42	157.5	4.3	706	1	NUCL_HUMAN	P19338 homo sapien
43	156.5	4.3	1332	1	SPT7_YEAST	P35177 saccharomyc
44	156.5	4.3	5596	1	MDN1_HUMAN	Q9nu22 homo sapien
45	156	4.3	1433	1	REST_CHICK	O42184 gallus gall

ALIGNMENTS

RESULT 1
A4_HUMAN
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q9BT38;
AC Q9UCB6; Q9UQ58;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";

RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [10]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [11]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [12]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [15]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [16]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [17]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [18]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [19]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [20]
RP SEQUENCE OF 672-681.
RC TISSUE=Brain cortex;
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [21]
RP SEQUENCE OF 674-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease.";

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  Query Match             98.3%;  Score 3590.5;  DB 1;  Length 770;
  Best Local Similarity   90.1%;  Pred. No. 3.2e-171;
  Matches  694;  Conservative    1;  Mismatches    0;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||||||||||||||||||||||||||||||||||||||||||              
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 ||||||||||||||| ||||||||||.|||||||||||||||.|||||.|||||| 
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 2
A4_MACFA
ID   A4_MACFA        STANDARD;      PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dabl (By similarity). Binding
CC       to Dabl inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
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CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL       1    17       BY SIMILARITY.
FT   CHAIN       18   770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN       18   687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN       18   671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN      672   770       C99 (POTENTIAL).
FT   CHAIN      672   713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN      672   711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN      688   770       C83 (POTENTIAL).
FT   CHAIN      688   713       P3(42) (POTENTIAL).
FT   CHAIN      688   711       P3(40) (POTENTIAL).
FT   CHAIN      712   770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN      714   770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN      721   770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN      740   770       C31 (POTENTIAL).
FT   DOMAIN      18   699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   700   723       POTENTIAL.
FT   DOMAIN     724   770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      96   110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     181   188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN     291   341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN     391   423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     491   522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     523   540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN     732   751       INTERACTION WITH G(O)-ALPHA
FT                              (BY SIMILARITY).
FT   DOMAIN     230   260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN     274   280       POLY-THR.
FT   SITE       144   144       REQUIRED FOR COPPER(II) REDUCTION
FT                              (BY SIMILARITY).
FT   ACT_SITE   301   302       REACTIVE BOND (BY SIMILARITY).
FT   SITE       671   672       CLEAVAGE (BY BETA-SECRETASE)
FT                              (BY SIMILARITY).
FT   SITE       672   673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE       687   688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                              (BY SIMILARITY).
FT   SITE       704   704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                              (BY SIMILARITY).
FT   SITE       706   706       INVOLVED IN OXIDATIVE REACTIONS
FT                              (BY SIMILARITY).
FT   SITE       711   712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                              (BY SIMILARITY).
FT   SITE       713   714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                              (BY SIMILARITY).
FT   SITE       720   721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                              (BY SIMILARITY).
FT   SITE       724   734       BASOLATERAL SORTING SIGNAL
FT                              (BY SIMILARITY).
FT   SITE       739   740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                              (BY SIMILARITY).
FT   SITE       757   760       ENDOCYTOSIS SIGNAL.
FT   SITE       759   762       NPXY MOTIF.

  Query Match            98.3%;  Score 3590.5;  DB 1;  Length 770;
  Best Local Similarity  90.1%;  Pred. No. 3.2e-171;
  Matches  694;  Conservative    1;  Mismatches    0;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLRKTTREPLIRD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
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Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 3
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amerim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
```

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CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      316    344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      363    428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      504    521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      713    732       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND.
FT   SITE        652    653       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        653    654       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        668    669       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        685    685       INVOLVED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        687    687       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        692    693       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        694    695       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        701    702       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                (BY SIMILARITY).
FT   SITE        705    715       BASOLATERAL SORTING SIGNAL
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                (BY SIMILARITY).
FT   SITE        738    741       ENDOCYTOSIS SIGNAL.
FT   SITE        740    743       NPXY MOTIF.
FT   METAL       137    137       COPPER (BY SIMILARITY).

  Query Match             98.2%;  Score 3584;  DB 1;  Length 751;
  Best Local Similarity   92.0%;  Pred. No. 6.6e-171;
  Matches  691;  Conservative    2;  Mismatches    2;  Indels   56;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||| ||||||||| |||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRDRKQCKTHPHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDHVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIAITTTTTTTESVEEVVR------------ 288
              |||||||||,|||||||||||||||||||||||||||||||||||||'||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ----------------------------------------------VPTTAASTPDAVDKYL 304
                                                           :|||||||||||||||
Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVIPTTAASTPDAVDKYL 360

Qy        305 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 364
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 420

Qy        365 ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR 424
              |||||||||||||||||,|||||||||||||||||||||||||||||||||||||||||||
Db        421 ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR 480

Qy        425 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ 484
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ 540

Qy        485 DEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 544
              |||||||||||||||||.||||:||||||||:||||||||||||||||||||||||||||
Db        541 DEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 600

Qy        545 PWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 660

Qy        605 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 720

Qy        665 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||
Db        721 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751


RESULT 4
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
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DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winterce A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dabl (By similarity). Binding
CC       to Dabl inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
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DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       C83 (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59).
FT   CHAIN       714    770       GAMMA-CTF(57).
FT   CHAIN       721    770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135    155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA (BY
FT                                SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).

  Query Match          96.8%;  Score 3535.5;  DB 1;  Length 770;
  Best Local Similarity  88.4%;  Pred. No. 1.7e-168;
  Matches  681;  Conservative    8;  Mismatches    6;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||:|||||.|||||.|||||||||||:||||:||||| ||| ||:||| |||
Db          1 MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |:| |||||||||||||||||||||||||||||||| || |||||| : ||||:|||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||:|||||||||||||||||:|||:|||||||||||||||| :|||||
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||:|||||||||||||||||||||||||||||||||||||||||||||
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Db        241 EAEDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLLKTTQEHLPQD 360

Qy        289 ---VPITAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||||||:||||:|||||||||||||||||||||||||||||:|||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 5
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
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RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apolipoproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clatherin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC       sulfate to the L-APP isoforms produces the APP proteoglycan core
CC       proteins, the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (BY SIMILARITY).

  Query Match             96.5%;  Score 3522.5;  DB 1;  Length 770;
  Best Local Similarity   88.2%;  Pred. No. 7.7e-168;
  Matches  679;  Conservative    7;  Mismatches    9;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              .|| ||:||| ||:||||||||||||||||||.|||||:||||||||||||||: |:||||
Db          1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWEPDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| :|||||||:||||:|||||||||||||||||||||||:|||||:||:||||||:|||
Db         61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||:||||||:||||:||||||||||||:||||:|||||.||||:||||||.|||  :||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |:|:||||.||||:|||||:||||||:|||||:||||||||||:||||| |||'.|:|:
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||:|||| :||||||::|||||||||||:||||||:|||||:||||:|||||||:
Db        241 EADDDEDVEDGDEVEEEAEEPYEEATEKTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RSMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQNLLKTSGEPVSQG 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||'||||:||||||:||||.|||'|:||||:.||||':|||:'||||'.|||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||:|||||:|.|||||||||||:|||||||:||||||||||||||:||||'||||:'|.
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||:|||||:|||||||||||||||||||||||||:|||||||.||| ||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              |||||||||||||||||:| ||||:|||||||:||||:|||||| |||:||||||'||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              ||||||||||||||||||||||| || |||||||||||||||||||||||||:|||||||.
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              |||||||||||||||||||:||'||||||||||||||||||.||||||||||||||||:::
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770


RESULT 6
A4_MOUSE
ID   A4_MOUSE       STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN [8]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [9]
RP SEQUENCE OF 656-737 FROM N.A.
RC STRAIN=129/Sv;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA Loring J.F., Goate A.M.;
RT "Introduction of six mutations into the mouse genome using 'Hit and
RT Run' gene-targeting: introduction of familial Alzheimer's disease
RT mutations into the mouse amyloid precursor protein gene and
RT humanization of the A-beta fragment.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX PubMed=8510506;
RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT "Regional distribution of the alternatively spliced isoforms of beta
RT APP RNA transcript in the brain of normal, heterozygous and
RT homozygous weaver mutant mice as revealed by in situ hybridization
RT histochemistry.";
RL Brain Res. Mol. Brain Res. 17:340-346(1993).
RN [11]
RP INTERACTION WITH KNS2.
RX PubMed=11144355;
RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT "Axonal transport of amyloid precursor protein is mediated by direct
RT binding to the kinesin light chain subunit of kinesin-I.";
RL Neuron 28:449-459(2000).
RN [12]
RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-726;
RP THR-743; TYR-757; ASN-759 AND TYR-762.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [13]
RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX MEDLINE=22028091; PubMed=11912189;
RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT with scaffold proteins of the JNK signaling cascade.";
RL J. Biol. Chem. 277:20070-20078(2002).
RN [14]
RP INTERACTION OF CTF PEPTIDES WITH NUMB.
RX PubMed=12011466;
RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT "The gamma-secretase-generated intracellular domain of beta-amyloid
RT precursor protein binds Numb and inhibits Notch signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN [15]
RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX PubMed=11553691;
RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT gamma-secretase is rapidly degraded but distributes partially in a
RT nuclear fraction of neurones in culture.";
RL J. Neurochem. 78:1168-1178(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions. Can promote transcription activation through binding
CC to APBB1/Tip60 and inhibit Notch signaling through interaction
CC with Numb. Couples to apoptosis-inducing pathways such as those
CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
CC similarity). Acts as a kinesin I membrane receptor, mediating the
CC axonal transport of beta-secretase and presenilin 1. May be
CC involved in copper homeostasis/oxidative stress through copper ion
CC reduction. Can regulate neurite outgrowth through binding to
CC components of the extracellular matrix such as heparin and
CC collagen I and IV (By similarity). The splice isoforms that
CC contain the BPTI domain possess protease inhibitor activity (By
CC similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis.
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC its serine phosphorylation. Also interacts with GPCR-like protein
CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC MT-binding domains (By similarity). Associates with microtubules
CC in the presence of ATP and in a kinesin-dependent manner (By
CC similarity). Interacts, through a C-terminal domain, with GNAO1
CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clatherin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 95.7%; Score 3493.5; DB 1; Length 770;
Best Local Similarity 87.8%; Pred. No. 2.1e-166;
Matches 676; Conservative 6; Mismatches 13; Indels 75; Gaps 1;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db 1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db 61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy 121 EPVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |:||||||||||:|:||||||||||||||||||||||||||:|||||||||||||.|:|.|
Db        181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||:'| |:||||||||||||||||||'||  |:||||'|.|||'|||
Db        241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGSVSTQSLLKTTSEPLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||:||||||||||||||||||||||||||||||||||||||||||'|||||' ||| |||
Db        361 PDKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              |:||||||||||||||||||||||||||||||||||:||||||:|||:|||:||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              |||||| ||||||||||||||||||||||||||||||||||||,|||:||||||||:|||'
Db        481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||:|||||||||||||||||||||||||||||||||:|||||:|||||'|||||'|:|||.|
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |:'||||.||||:||||||:| || ||||||| ||||: |||||| |||:'||||:: |||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              :||||:||||||||| ||'|:|| ||||||:|||:|||||||||:|||| :||||:|||
Db        661 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||:|||||||:||||||:||||||||||||||'|||||||||:|||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 7
A4_RAT
ID   A4_RAT   STANDARD;   PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE   amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE   C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE   fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE   Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN   APP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88312583; PubMed=2900758;
RA   Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA   Seeburg P.H.;
RT   "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT   in rat brain suggests a role in cell contact.";
RL   EMBO J. 7:1365-1370(1988).
RN   [2]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89183625; PubMed=2648331;
RA   Kang J., Mueller-Hill B.;
RT   "The sequence of the two extra exons in rat preA4.";
RL   Nucleic Acids Res. 17:2130-2130(1989).
RN   [3]
RP   SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX   PubMed=11483588;
RA   Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT   "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT   family resembling gamma-secretase-like cleavage of Notch.";
RL   J. Biol. Chem. 276:35235-35238(2001).
RN   [4]
RP   ALTERNATIVE SPLICING.
RX   PubMed=8624099;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "APP gene family. Alternative splicing generates functionally related
RT   isoforms.";
RL   Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN   [5]
RP   TISSUE SPECIFICITY OF APPICAN.
RX   PubMed=7744833;
RA   Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA   Mytilineou C., Margolis R.U., Robakis N.K.;
RT   "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT   brain and is produced by astrocytes but not by neurons in primary
RT   neural cultures.";
RL   J. Biol. Chem. 270:11839-11844(1995).
RN   [6]
RP   TISSUE SPECIFICITY OF ISOFORMS.
RX   PubMed=8996834;
RA   Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT   "Expression of the APP gene family in brain cells, brain development
RT   and aging.";
RL   Gerontology 43:119-131(1997).
RN   [7]
RP   INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP   TYR-762.
RX   PubMed=9930726;
RA   Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA   Suzuki T., Nairn A.C., Greengard P.;
RT   "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT   Alzheimer's amyloid precursor protein.";
RL   J. Neurochem. 72:549-556(1999).
RN   [8]
RP   INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND HIS-733.
RX   PubMed=10024358;
RA   Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA   Valenza C., Prochiantz A., Allinquant B.;
RT   "The amyloid precursor protein interacts with Go heterotrimeric
RT   protein within a cell compartment specialized in signal
RT   transduction.";
RL   J. Neurosci. 19:1717-1727(1999).
RN   [9]
RP   CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX   MEDLINE=95256193; PubMed=7737970;
RA   Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT   "The chondroitin sulfate attachment site of appican is formed by
RT   splicing out exon 15 of the amyloid precursor gene.";
RL   J. Biol. Chem. 270:10388-10391(1995).
RN   [10]
RP   BETA-AMYLOID METAL-BINDING.
RX   PubMed=10386999;
RA   Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA   Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA   Bush A.I.;
RT   "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT   peroxide through metal ion reduction.";
RL   Biochemistry 38:7609-7616(1999).
RN   [11]
RP   BETA-AMYLOID ZINC BINDING.
RX   MEDLINE=99343552; PubMed=10413512;

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RA   Liu S.T., Howlett G., Barrow C.J.;
RT   "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT   of the A beta peptide of Alzheimer's disease.";
RL   Biochemistry 38:9373-9378(1999).
RN   [12]
RP   IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP   GLY-704.
RX   PubMed=11959460;
RA   Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT   "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT   peptide 1-42-associated oxidative stress and neurotoxicity.";
RL   Biochim. Biophys. Acta 1586:190-198(2001).
RN   [13]
RP   PHOSPHORYLATION.
RX   PubMed=9085254;
RA   Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA   Greengard P., Suzuki T.;
RT   "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT   phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT   cultured cells.";
RL   Mol. Med. 3:111-123(1997).
RN   [14]
RP   PHOSPHORYLATION ON SER-730.
RX   PubMed=10329382;
RA   Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA   Greengard P., Nairn A.C., Suzuki T.;
RT   "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT   precursor protein at Ser655 by a novel protein kinase.";
RL   Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN   [15]
RP   PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP   THR-743.
RX   MEDLINE=99274744; PubMed=10341243;
RA   Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA   Kirino Y., Greengard P., Suzuki T.;
RT   "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT   during neuronal differentiation.";
RL   J. Neurosci. 19:4421-4427(1999).
RN   [16]
RP   PHOSPHORYLATION ON THR-743.
RX   PubMed=10936190;
RA   Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA   Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT   "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT   protein by cyclin-dependent kinase 5.";
RL   J. Neurochem. 75:1085-1091(2000).
RN   [17]
RP   CARBOHYDRATE STRUCTURE OF APPICAN.
RX   PubMed=11479316;
RA   Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA   Sugahara K., Robakis N.K.;
RT   "Appican, the proteoglycan form of the amyloid precursor protein,
RT   contains chondroitin sulfate E in the repeating disaccharide region
RT   and 4-O-sulfated galactose in the linkage region.";
RL   J. Biol. Chem. 276:37155-37160(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC       G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC       mediating the axonal transport of beta-secretase and presenilin 1
CC       (By similarity). May be involved in copper homeostasis/oxidative
CC       stress through copper ion reduction. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I and IV (By similarity). The
CC       splice isoforms that contain the BPTI domain possess protease
CC       inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain.
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dabl (By similarity). Binding
CC       to Dabl inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity). Interacts,
CC       through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC       CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC       associates with HADH2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the

  Query Match             95.7%;  Score 3493.5;  DB 1;  Length 770;
  Best Local Similarity   87.7%;  Pred. No. 2.1e-166;
  Matches  675;  Conservative    8;  Mismatches   12;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| ||||||||||||||||||||||:|:||||||||:|:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTITTTTTESVEEVVR---------- 288
              ||:|||| |||||||||||||||||||||||||||||||||||||||||
Db        241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVSSQSLLKTTSEPLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                  :||||||||,||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPITAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
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Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645

Db        661 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770


RESULT 8
APP2_MOUSE
ID   APP2_MOUSE     STANDARD;      PRT;   695 AA.
AC   Q06335;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).
GN   APLP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RA   von der Kammer H.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-246 FROM N.A.
RX   MEDLINE=94032480; PubMed=8218408;
RA   Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;
RT   "The complete cDNA coding sequence for the mouse CDEI binding
RT   protein.";
RL   Biochim. Biophys. Acta 1216:154-156(1993).
RN   [3]
RP   SEQUENCE OF 185-695 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Heart;
RX   MEDLINE=93129193; PubMed=1482349;
RA   Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
RT   "A murine sequence-specific DNA binding protein shows extensive local
RT   similarities to the amyloid precursor protein.";
RL   Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
RN   [4]
RP   SEQUENCE OF 1-35 FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=96029629; PubMed=7592716;
RA   von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
RA   Gilbert D.J., Jenkins N.A., Sisodia S.S.;
RT   "The mouse APLP2 gene. Chromosomal localization and promoter
RT   characterization.";
RL   J. Biol. Chem. 270:25475-25480(1995).
CC   -!- FUNCTION: BINDS TO THE DNA 5'-GTCACATG-3'(CDEI BOX) WHICH PLAYS
CC       AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC       (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z22592; CAA80306.1; -.
DR   EMBL; M97216; AAA20039.1; -.
DR   EMBL; U34291; AAC52318.1; -.
DR   PIR; S38344; S38344.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88047; Aplp2.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Transmembrane; DNA-binding; Signal; Nuclear protein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    695       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    624       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    625    648       POTENTIAL.
FT   DOMAIN      649    695       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    294       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      218    231       POLY-GLU.
FT   DOMAIN      256    266       POLY-GLU.
FT   CARBOHYD    485    485       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    185    189       GMLLP -> MACCC (IN REF. 3).
SQ   SEQUENCE   695 AA;  78944 MW;  BBF4B95AAB2A0311 CRC64;

  Query Match             47.5%;  Score 1735;  DB 1;  Length 695;
  Best Local Similarity   49.3%;  Pred. No. 3.3e-79;
  Matches  360;  Conservative  118;  Mismatches  162;  Indels   90;  Gaps   19;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56

Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116

Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176

Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE---E 231

Db        193 DQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------OEEDEEEDYDLDKSEFPTE 243

Qy        232 EEVAEVEEEEAD-DDEDDEDGDEVEEEAE--------EPYEEATERTTSIAITTTTTTES 282

Db        244 ADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTISDKE 301

Qy        283 VEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAE 342

Db        302 IVHDVKVPPTPLPTND-VDVYLETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAE 360

Qy        343 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYI 402

Db        361 LQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYL 420

Qy        403 TALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 462

Db        421 AALQSDPPRPRHRILQAERRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVI 480

Qy        463 YERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSL 522

Db        481 EERRNQSLTLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFISSI 523

Qy        523 TETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSG 582

Db        524 SENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQDG-G 566

Qy        583 LTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NK 624

Db        567 LIGAEEKVINSKNKMDENMVIDETLDV--KEM1FNAERVGGLEEEPESVGPLREDFSLSS 624

Qy        625 GAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYEN 684

Db        625 NALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYEN 684

Qy        685 PTYKFFEQMQ 694
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                    ||||: ||||
Db        685 PTYKYLEQMQ 694


RESULT 9
APP2_HUMAN
ID   APP2_HUMAN     STANDARD;      PRT;   763 AA.
AC   Q06481;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE   (CDE1-box binding protein) (CDEBP).
GN   APLP2 OR APPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=93250009; PubMed=8485127;
RA   Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA   Norris K., Foster D.C.;
RT   "Molecular cloning of the cDNA for a human amyloid precursor protein
RT   homolog: evidence for a multigene family.";
RL   Biochemistry 32:4481-4486(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=95217334; PubMed=7702756;
RA   von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
RT   "A human amyloid precursor-like protein is highly homologous to a
RT   mouse sequence-specific DNA-binding protein.";
RL   DNA Cell Biol. 13:1137-1143(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94035131; PubMed=8220435;
RA   Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA   Hyman B.T., Neve R.L., Tanzi R.E.;
RT   "Isolation and characterization of APLP2 encoding a homologue of the
RT   Alzheimer's associated amyloid beta protein precursor.";
RL   Nat. Genet. 5:95-99(1993).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC       SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC       FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC       MAY BIND TO THE DNA 5'-GTCACATG-3'(CDE1 BOX).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC       (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=Q06481-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q06481-2; Sequence=VSP_000018;
CC       Name=3;
CC         IsoId=Q06481-3; Sequence=VSP_000019;
CC   -!- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
CC       AND ENDOTHELIAL TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S60099; AAC60589.1; -.
DR   EMBL; L09209; AAA35526.1; -.
DR   EMBL; Z22572; CAA80295.1; -.
DR   EMBL; L27631; AAC41701.1; -.
DR   EMBL; BC000373; AAH00373.1; -.
DR   PIR; A49321; A49321.
DR   HSSP; P05067; 1MWP.
DR   Genew; HGNC:598; APLP2.
DR   MIM; 104776; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0003677; F:DNA binding activity; NAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Signal; Alternative splicing; DNA-binding;
KW   Nuclear protein; Serine protease inhibitor.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    763       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    692       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    693    716       POTENTIAL.
FT   DOMAIN      717    763       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      215    280       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      306    364       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      215    231       POLY-GLU.
FT   ACT_SITE    320    321       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    310    360       BY SIMILARITY.
FT   DISULFID    319    343       BY SIMILARITY.
FT   DISULFID    335    356       BY SIMILARITY.
FT   VARSPLIC    308    363       Missing (in isoform 2).
FT                                /FTId=VSP_000018.
FT   VARSPLIC    613    624       Missing (in isoform 3).
FT                                /FTId=VSP_000019.
FT   CONFLICT    543    543       S -> I (IN REF. 1).
SQ   SEQUENCE   763 AA;  86955 MW;  CA3A7D6DDB8A28D0 CRC64;

  Query Match             47.3%;  Score 1728;  DB 1;  Length 763;
  Best Local Similarity   47.1%;  Pred. No. 8.1e-79;
  Matches  372;  Conservative  112;  Mismatches  165;  Indels  140;  Gaps   20;
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Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
                | ||||   :| ||  :            |||     :|'.:|||||:':||'|:|:|   ||: :
Db         15 LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              ::||:| :||| :|:|||:|:||||!|:||:| |:| |.|:| : |||:     || ::
Db         75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||:|| |||:||:| ':|||:'|| | ||||| || |   :    |: |||'':||:
Db        133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:||||  :     :!    : |||:        ' : :  |  ||  :  :|    |:
Db        193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-------EEEEEDEEEDYDVYKSEFPTEAD 245

Qy        237 VEE--EEA--DDDEDDEDGDEVEEEAEEPY----------EEATERTTSIATTTTTTTES 282
              :|:  : |  :||||:|:|:|| |: :  |            | ||  :    :   |
Db        246 LEDFTEAAVDEDDEDEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy        283 VEEV----------------------------------------------------VRVP 290
              |: |                                                     :|
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMIP 365

Qy        291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPK 350
               |    | | :| | !|   |:|:|| ||||||:|| :|| |. :| :|||||   ||.'|||
Db        366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy        351 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPP 410
              |::: :|||||  |::||:|||:|:||||||:||||||||||||:|||||: ||': |.
Db        425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP 484

Qy        411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 470
              ||  :     |::||||| :|| ||::|::||  |||: |||::'|||||, || ·| |||,
Db        485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSL 544

Qy        471 SLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVE 530
              ||:| || ||:|||:|:||||||:::           |::            :      |::||    |
Db        545 SLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTASISETPVDVR 587

Qy        531 LLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLITRPGSGLTN----- 585
                 |: | | ::: :| |        |:  |||      | :|          :   :  ..:: 
Db        588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGGL 635

Qy        586 IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----------------NKG 625
              |  ||      |: |:|         |       ::    ::::| || .|                 :
Db        636 IGAEEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEEERESVGPLREDFSLSSS 693

Qy        626 AIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENP 685
              |:||:|:|    ' ||||'||:||||:|:|| :| ||:||||   ::|||  ·|:||| :||
Db        694 ALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENP 753

Qy        686 TYKFFEQMQ 694
              ||.: ||:
Db        754 TYKYLEQMQ 762
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RESULT 10
APP2_RAT
ID   APP2_RAT      STANDARD;      PRT;   765 AA.
AC   P15943;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
GN   APLP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-627 FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain, and Heart;
RX   MEDLINE=94368849; PubMed=8086458;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT   protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT   difference to human and murine homologues.";
RL   Biochim. Biophys. Acta 1219:167-170(1994).
RN   [2]
RP   SEQUENCE OF 575-765 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=90207205; PubMed=1690887;
RA   Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT   "Characterization of cDNA encoding a human sperm membrane protein
RT   related to A4 amyloid protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=P15943-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=P15943-2; Sequence=VSP_000021;
CC       Name=C;
CC         IsoId=P15943-3; Sequence=VSP_000020;
CC       Name=D;
CC         IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X77934; CAA54906.1; -.
DR   EMBL; M31322; AAA42352.1; -.
DR   PIR; A35981; A35981.
DR   PIR; S42880; S42880.
DR   HSSP; P05067; 1MWP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Alternative splicing; Serine protease inhibitor;
KW   Signal; Glycoprotein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    765       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    695       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    696    718       POTENTIAL.
FT   DOMAIN      719    765       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    282       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      308    366       BPTI/KUNITZ INHIBITOR.
FT   ACT_SITE    322    323       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    312    362       BY SIMILARITY.
FT   DISULFID    321    345       BY SIMILARITY.
FT   DISULFID    337    358       BY SIMILARITY.
FT   DOMAIN      218    229       POLY-GLU.
FT   CARBOHYD    628    628       O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT   VARSPLIC    311    365       Missing (in isoform C and isoform D).
FT                                /FTId=VSP_000020.
FT   VARSPLIC    616    627       Missing (in isoform B and isoform D).
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FT                                /FTId-VSP_000021.
FT   CONFLICT    575    577       DQF -> EFV (IN REF. 2).
SQ   SEQUENCE   765 AA;  86882 MW;  CF51FCCCE305A0CF CRC64;

  Query Match              47.0%;  Score 1716;  DB 1;  Length 765;
  Best Local Similarity    46.2%;  Pred. No. 3.2e-78;
  Matches  364;  Conservative  122;  Mismatches  166;  Indels  136;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----FTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
Db        133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYA-DGSEDKVVEVAEEEE 233
Db        193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEE----DEEEDYALDKSEFPTEADLEDFT 248

Qy        234 VAEVEEEEADDDEDDEDGDEVEEEAEEPYEE------ATERTTSIATTTTTTTESVEEVV 287
Db        249 EAAADEDEDEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV 308

Qy        288 R-------------------------------------------------------VPT 291
Db        309 KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMIPP 368

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
Db        369 TPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRSRMDRVKKEWEEAELQAKNLPKA 427

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
Db        428 ERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYLAALQSDPPR 487

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
Db        488 PHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSLS 547

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
Db        548 LLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSSISENPVDVR- 589

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN-----I 586
Db        590 --VSSEES-EEIPPFHPF--HPFPSLSENE----DTQPELYHPM--KKGSGMAEQDGGLI 638

Qy        587 KTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----------------NKGA 626
Db        639 GAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPDSVGPLREDFSLSSSA 696

Qy        627 IIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPT 686
Db        697 LIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPMLTPEERHLNKMQNHGYENPT 756

Qy        687 YKFFEQMQ 694
Db        757 YKYLEQMQ 764
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RESULT 11
APP1_HUMAN
ID   APP1_HUMAN     STANDARD;      PRT;   650 AA.
AC   P51693; O00113; Q96A92;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN   APLP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98088960; PubMed=9428684;
RA   Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L., Multhaup G.,
RA   Masters C.L., Beyreuther K., Weidemann A.;
RT   "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
RT   expression in COS-7 cells and identification of soluble forms in the
RT   cerebrospinal fluid.";
RL   Eur. J. Biochem. 250:354-363(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98180887; PubMed=9521588;
RA   Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
RA   Olsen A., Tryggvason K.;
RT   "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT   19q13.1.";
RL   Hum. Genet. 102:192-196(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
RX   MEDLINE=96115107; PubMed=7494461;
RA   Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
RA   Black I.B.;
RT   "Selective localization of amyloid precursor-like protein 1 in the
RT   cerebral cortex postsynaptic density.";
RL   Brain Res. Mol. Brain Res. 32:36-44(1995).
RN   [5]
RP   HEPARIN AND ZINC BINDING.
RX   MEDLINE=95014513; PubMed=7929392;
RA   Bush A.I., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RT   "The amyloid beta-protein precursor and its mammalian homologues.
RT   Evidence for a zinc-modulated heparin-binding superfamily.";
RL   J. Biol. Chem. 269:26618-26621(1994).
RN   [6]
RP   INTERACTION WITH APBA2.
RX   MEDLINE=99107877; PubMed=9890987;
RA   Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA   Sakiyama S., Kirino Y., Suzuki T.;
RT   "Interaction of a neuron-specific protein containing PDZ domains with
RT   Alzheimer's amyloid precursor protein.";
RL   J. Biol. Chem. 274:2243-2254(1999).
RN   [7]
RP   EXTRACELLULAR COPPER-BINDING.
RX   MEDLINE=22130992; PubMed=12135352;
RA   Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,
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RA   Reed J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
RA   Bayer T.A., Multhaup G.;
RT   "Evidence for a copper-binding superfamily of the amyloid precursor
RT   protein.";
RL   Biochemistry 41:9310-9320(2002).
CC   -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC       gamma-secretase processed fragment, AlCD1, activates transcription
CC       activation through APBB1 (Fe65) binding (By similarity). Couples
CC       to JIP signal transduction through C-terminal binding. May
CC       interact with cellular G-protein signaling pathways. Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I.
CC   -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC       neuronal apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB and APBA family members,
CC       MAPK8IP1 and Dabl (By similarity). Binding to Dabl inhibits its
CC       serine phosphorylation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC       processed in the Golgi complex.
CC   -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
CC       localized to the postsynaptic density (PSD).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The NPXY site is also involved in clatherin-mediated
CC       endocytosis.
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal
CC       apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
CC       similarity).
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: O-glycosylated.
CC   -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC       Zinc-binding increases heparin binding. No Cu(II) reducing
CC       activity with copper-binding.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U48437; AAB96331.1; -.
DR   EMBL; AD000864; AAB50173.1; -.
DR   EMBL; BC012889; AAH12889.1; -.
DR   HSSP; P05067; 1MWP.
DR   Genew; HGNC:597; APLP1.
DR   MIM; 104775; -.
DR   GO; GO:0005604; C:basement membrane; TAS.
DR   GO; GO:0005208; F:amyloid protein; TAS.
DR   GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR   GO; GO:0007399; P:neurogenesis; TAS.
DR   InterPro; IPR001866; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW   Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW   Glycoprotein.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    650       AMYLOID-LIKE PROTEIN 1.
FT   CHAIN       621    650       C30 (BY SIMILARITY).
FT   DOMAIN       39    580       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    581    603       POTENTIAL.
FT   DOMAIN      604    650       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      158    178       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      204    211       ZINC-BINDING.
FT   DOMAIN      310    342       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      410    441       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      442    459       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      640    643       CLATHRIN-BINDING (POTENTIAL).
FT   DOMAIN      241    247       POLY-GLU.
FT   DOMAIN      264    268       POLY-GLU.
FT   SITE        167    167       REQUIRED FOR COPPER(II) REDUCTION (BY
FT                                SIMILARITY).
FT   SITE        604    615       BASOLATERAL SORTING SIGNAL (BY
FT                                SIMILARITY).
FT   SITE        620    621       CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT   SITE        638    641       ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT   SITE        640    643       NPXY MOTIF.
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    461    461       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    551    551       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     48     48       A -> P (IN REF. 1).
SQ   SEQUENCE   650 AA;  72176 MW;  B95F0F4D1C5CBAC7 CRC64;

  Query Match             32.6%;  Score 1190;  DB 1;  Length 650;
  Best Local Similarity   38.8%;  Pred. No. 3.3e-52;
  Matches  272;  Conservative  115;  Mismatches  230;  Indels   84;  Gaps   16;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              :|| | ||| |     :|   : | |      |:|  |||| :| ::: |:|: || ::
Db         23 LLPLLLLLLRAQPAIGSLAGGSPGAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRSR 82

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCLV 119
               |:   : :|:|||:::|||||  | :| | : :: ||   |     ||| |:|:|||
Db         83 RCLRDPQRVLEYCRQMYPELQIARVEQATQAIPMERWCGGSRSGSCAHPHHQVVPFRCLP 142

Qy        120 GEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKF 179
              |||||:|||||: |:|||||||| ||:    |  |:| || :   ||  |||||'| |:|
Db        143 GEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDRF 202

Qy        180 RGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEE 239
              ||||:|||||     |   | |  | |  |         :|    |: ||:||    ||
Db        203 RGVEYVCCPPPCTPD--PSGTAVGDPSTRSW-------PPGSR---VEGAEDEE----EE 246

Qy        240 EEADDDEDD--EDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTIAASTP 297
              |      ||   :  :|| ||      :  | ::    | |          ||
Db        247 ESFPQPVDDYFVEPPQAEEE-EETVPPPSSHTLAVVGKVTPTPR--------PT------ 291

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              | |: |   ||: :||  | :|:  || :   ::::|||||  |: |:|||||||::|:
Db        292 DGVDIYFGMPGEISEHEGFLRAKMDLEERRMRQINEVMREWAMADNQSKNLPKADRQALN 351

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              :|||  :::||:: : |||:|||||  || |::||:|| ||| :: |||| ||:   |
Db        352 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQADPPQAERVLL 411

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |::|:||||:::|||:|::||  |||:|| |:| || |||:|| ||:|:|| !!   |
Db        412 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVHTHLQVIEERVNQSLGLLDQNP 471

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTEIKTTVELLPVNGE 537
              :|: :: :: |||  |                    | ||  |        | |
Db        472 HLAQELRPQIQELLHSEH----------------------LGPSELEA-------PAPGG 502

Qy        538 FSLD--DLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVK 595
              | |   |||  |   | |                    :| | :  :      |   : : :
Db        503 SSEDKGGLQPPDS--KDDTPM------------TLPKGSTEQDAASPEKEKMNPLEQYE 547

Qy        596 MDAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML-KKK 651
                    |:  |    |:       | :: |: ||:: |    :::|:::::| :||
Db        548 RKVNASVPRGFPFHSSEIQRDELAPAGTGVSREAVSGLLIMGAGGGSLIVLSMLLLRRKK 607

Qy        652 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
              | :| |||||||  :| || : ::|::|||||||:| |:
Db        608 PYGAISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 648


RESULT 12
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APP1_MOUSE
ID   APP1_MOUSE     STANDARD;      PRT:   653 AA.
AC   Q03157; Q8VC38;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 1 precursor (APLP) (APLP-1) (Contains: C30).
GN   APLP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=93066322; PubMed=1279693;
RA   Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
RA   Solomon F.;
RT   "Identification of a mouse brain cDNA that encodes a protein related
RT   to the Alzheimer disease-associated amyloid beta protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   COLLAGEN-BINDING.
RX   MEDLINE=96139497; PubMed=8576160;
RA   Beher D., Hesse L., Masters C.L., Multhaup G.;
RT   "Regulation of amyloid protein precursor (APP) binding to collagen and
RT   mapping of the binding sites on APP and collagen type I.";
RL   J. Biol. Chem. 271:1613-1620(1996).
RN   [4]
RP   INTERACTION WITH DAB1.
RX   MEDLINE=99389880; PubMed=10460257;
RA   Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT   "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RT   protein 1.";
RL   J. Neurosci. 19:7507-7515(1999).
RN   [5]
RP   INTERACTION WITH MAPK8IP1.
RX   MEDLINE=21408156; PubMed=11517249;
RA   Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA   Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA   Kyriakis J.M., Nishimoto I.;
RT   "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT   scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL   J. Neurosci. 21:6597-6607(2001).
RN   [6]
RP   GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
RP   TYR-641.
RX   MEDLINE=22313598; PubMed=12228233;
RA   Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
RT   "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RT   secretase regulates transcription.";
RL   J. Biol. Chem. 277:44195-44201(2002).
CC   -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC       gamma-secretase processed fragment, ALID1, activates transcription
CC       activation through APBB1 (Fe65) binding. Couples to JIP signal
CC       transduction through C-terminal binding. May interact with
CC       cellular G-protein signaling pathways. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I.
CC   -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC       neuronal apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB and APBA family members,
CC       MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC       serine phosphorylation.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC       processed in the Golgi complex.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The NPXY site is also involved in clatherin-mediated
CC       endocytosis.
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal
CC       apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC       similarity).
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: O-glycosylated.
CC   -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC       Zinc-binding increases heparin binding. No Cu(II) reducing
CC       activity with copper-binding.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L04538; AAA37247.1; -.
DR   EMBL; BC021877; AAH21877.1; -.
DR   PIR; A46362; A46362.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88046; Aplp1.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW   Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW   Glycoprotein.
FT   SIGNAL        1     37       POTENTIAL.
FT   CHAIN        38    653       AMYLOID-LIKE PROTEIN 1.
FT   CHAIN       624    653       C30 (BY SIMILARITY).
FT   DOMAIN       38    583       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    584    606       POTENTIAL.
FT   DOMAIN      607    653       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      157    177       COPPER-BINDING.
FT   DOMAIN      203    210       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      313    345       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      413    444       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      445    462       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      263    271       POLY-GLU.
FT   DOMAIN      535    538       POLY-SER.
FT   DOMAIN      601    606       POLY-LEU.
FT   SITE        166    166       REQUIRED FOR COPPER(II) REDUCTION (BY
FT                                SIMILARITY).
FT   SITE        607    618       BASOLATERAL SORTING SIGNAL (BY
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FT                                SIMILARITY).
FT   SITE        623     624      CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT   SITE        641     644      ENDOCYTOSIS SIGNAL.
FT   SITE        643     646      NPXY MOTIF.
FT   CARBOHYD    464     464      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    554     554      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MUTAGEN     641     641      Y->G: REDUCED BINDING OF APBB1.
FT   CONFLICT     17      17      P -> PP (IN REF. 2).
SQ   SEQUENCE   653 AA;  72750 MW;  56516DC3EA40E4#0 CRC64;

  Query Match             32.5%;  Score 1185;  DB 1;  Length 653;
  Best Local Similarity   38.6%;  Pred. No. 5.8e-52;
  Matches  270;  Conservative  121;  Mismatches  231;  Indels   78;  Gaps   17;

Qy          1 MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGT 59
              :|| |:|||| |  |     | :  |      |:  ||| :| ::: |:,: |,  :
Db         22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy         60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
              : |:   : :|:|||:::|-|| |  | :| | : :: :'   |      ||| ':|: |:
Db         81 RRCLLDPQRVLEYCRQMYPELHIARVFQAAQAIPMERWCGGIRSGRCAHPHHEVVPFHCL 140

Qy        119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
              |||||:|||||: |:|||||||| ||:    |  :|| || :   |:  |:,||  |:
Db        141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLIIHGSGMLLPCGSDR 200

Qy        179 FRGVEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
              |||||:|||    : |    | :  :  |  ||     |:|  |       |:,|
Db        201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-------EEEVESF 248

Qy        238 EEEEADDDEDDEDGDEVEEEAEEPYEEATERITSIATTTTTTTESVEEVVRVPTTAASTP 297
              :  |   :    :| ||| ||      :  |  : :  | |           ||
Db        249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR--------PT------ 294

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              | || |   ||:  ||  | :|'  || :   :::|||||  |: |:||||''|:::
Db        295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354

Qy        358 QHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVPN 417
              :|||  :::||:: : |||:|||||  || |:::|||:|| ||| :: |||  ||:   |
Db        355 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              :::|:|||||:::|||:|:||  |||:|| |:: || ||'|:|| .'||||| ||   ,
Db        415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
              :|:|:: :: |!!          ||  :    :    |  :| | :| :
Db        475 HLAQELRPQIQELL----------LAEHLGPSEL----DASVPGSSSEDK---------- 510

Qy        537 EFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
                  '|,|             |:: :|    |   :: | :  |     |   : : :
Db        511 ----GSLQP-----------PESKDDPPVTLP---KGSTDQFSSSSGREKLTPLEQYFQ 551

Qy        597 DAEPRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML-KKKQ 652
                  |:  |    ::         | :: |:  .:: '    ::#|::|::| | '
Db        552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSLIVLSLLLLRKKKP 611

Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
              : :| |:|||||  :| |:: | ::::::|||.|:|:| ::
Db        612 YGTISHGVVEVDPMLTLEEQQLREMQRHGYENPTYRFLEE 651


RESULT 13
A4_CAEEL
ID   A4_CAEEL       STANDARD;      PRT:   686 AA.
AC   Q10651; Q18583; Q95ZX1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-amyloid-like protein precursor.
GN   APL-1 OR C42D8.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE OF 6-686 FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=94089766; PubMed=8265668;
RA   Daigle I., Li C.;
RT   "apl-1, a Caenorhabditis elegans gene encoding a protein related to
RT   the human beta-amyloid protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:12045-12049(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Hallsworth K.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   REVISIONS, AND ALTERNATIVE SPLICING.
RA   Waterston R.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=a;
CC         IsoId=Q10651-1; Sequence=Displayed;
CC       Name=b;
CC         IsoId=Q10651-2; Sequence=VSP_000017;
CC         Note=No experimental confirmation available;
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U00240; AAC46470.1; ALT_INIT.
DR   EMBL; U56966; AAA98722.1; -.
DR   EMBL; U56966; AAK68242.1; -.
DR   PIR; T15795; T15795.
DR   HSSP; P05067; 1MWP.
DR   WormPep; C42D8.8a; CE04209.
DR   WormPep; C42D8.8b; CE27845.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
KW   Signal; Transmembrane; Amyloid; Neurogenesis; Glycoprotein;
KW   Alternative splicing.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    686       BETA-AMYLOID-LIKE PROTEIN.
FT   DOMAIN       22    621       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    622    642       POTENTIAL.
FT   DOMAIN      643    686       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      205    228       ASP-RICH.
FT   DOMAIN      676    679       CLATHRIN-BINDING (POTENTIAL).
FT   CARBOHYD     84     84       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    538    539       Missing (in isoform b).
FT                                /FTId=VSP_000017.
SQ   SEQUENCE   686 AA;  79434 MW;  A0816858FDD48608 CRC64;

  Query Match             22.4%;  Score 817.5;  DB 1;  Length 686;
  Best Local Similarity   29.1%;  Pred. No. 1.1e-33;
  Matches  222;  Conservative  110;  Mismatches  275;  Indels  155;  Gaps   22;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              :: || : :| | |  |  |          | :|  ||  | :|  : | :|
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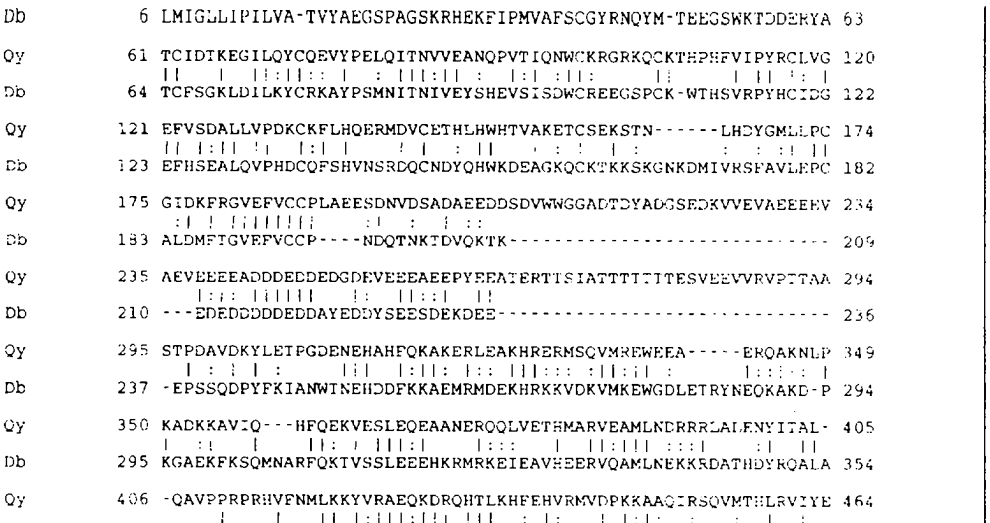

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RESULT 14
A4_DROME
ID   A4_DROME       STANDARD;      PRT;   887 AA.
AC   P14599; Q9IVV0; Q9U4H3; Q9W5F1;
DT   01-APR-1990 (Rel. 14, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-amyloid-like protein precursor.
GN   APPL OR VND OR BCDNA:GH04413 OR EG:65F1.5 OR CG7727.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89184650; PubMed=2494667;
RA   Rosen D.R., Martin-Morris L., Luo L., White K.;
RT   "A Drosophila gene encoding a protein resembling the human
RT   beta-amyloid protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [3]
RP   REVISIONS.
RC   STRAIN=Berkeley;
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Oregon-R;
RX   MEDLINE=20196011; PubMed=10731137;
RA   Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA   Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA   Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA   Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA   Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA   Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
RA   Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
RA   Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA   McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA   Glover D.M.;
RT   "From sequence to chromosome: the tip of the X chromosome of D.
RT   melanogaster.";
RL   Science 287:2220-2222(2000).
RN   [5]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley; TISSUE=Ovary;
RX   MEDLINE=20196012; PubMed=10731138;
RA   Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
RA   Stapleton M., Harvey D.A.;
RT   "A Drosophila complementary DNA resource.";
RL   Science 287:2222-2224(2000).
RN   [6]
RP   SEQUENCE OF 1-83 FROM N.A.
RX   MEDLINE=91184006; PubMed=2127912;
RA   Martin-Morris L.E., White K.;
RT   "The Drosophila transcript encoded by the beta-amyloid protein
RT   precursor-like gene is restricted to the nervous system.";
RL   Development 110:185-195(1990).
CC   -!- FUNCTION: Probably corresponds to the protein encoded by the
CC       essential locus vnd, a gene required for embryonic nervous system
CC       development.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in post-mitotic neurons in the
CC       central and peripheral nervous systems. Within the nervous system
CC       transcripts are not observed in neuroblasts, newly generated
CC       neurons and at least one class of presumed glial cells.
CC   -!- DEVELOPMENTAL STAGE: Expressed in all developmental stages.
CC   -!- DOMAIN: The clathrin-binding site is essential for its association
CC       with xl1-alpha, -beta, and -gamma. The sequence specific
CC       recognition extends to peptide residues that are C-terminal to the
CC       NPXY motif. This interaction appears to be independent of
CC       phosphorylation (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; J04516; AAA28874.1; -.
DR   EMBL; AE003418; AAF45520.2; -.
DR   EMBL; AL031883; CAA21409.1; -.
DR   EMBL; AL022139; CAA21409.1; JOINED.
DR   EMBL; AL022139; CAA18093.1; -.
DR   EMBL; AL031883; CAA18093.1; JOINED.
DR   EMBL; AF181628; AAD55414.1; -.
DR   EMBL; X55774; CAA39294.1; -.
DR   EMBL; X55775; CAA39294.1; JOINED.
DR   PIR; A32758; A32758.
DR   HSSP; P05067; 1MWP.
DR   FlyBase; FBgn0000108; Appl.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   InterPro; IPR001968; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal; Transmembrane; Amyloid; Neurogenesis.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    887       BETA-AMYLOID-LIKE PROTEIN.
FT   DOMAIN       28    813       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    814    834       POTENTIAL.
FT   DOMAIN      835    887       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      877    880       CLATHRIN-BINDING (POTENTIAL).
FT   CARBOHYD    150    150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    237    237       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    240    240       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    574    574       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    177    177       S -> T (IN REF. 1).
FT   CONFLICT    229    229       MISSING (IN REF. 1).
FT   CONFLICT    332    332       V -> M (IN REF. 4).
FT   CONFLICT    743    743       S -> T (IN REF. 1).

SQ   SEQUENCE   887 AA;  98332 MW;  F0FC855AD65A5275 CRC64;

  Query Match             20.5%;  Score 748.5;  DB 1;  Length 887;
  Best Local Similarity   25.5%;  Pred. No. 3.6e-30;
  Matches  233;  Conservative  128;  Mismatches  287;  Indels  265;  Gaps   29;

Qy          7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDSDPSG 58
              ||| : |   |:     | | : |     |||||: |  |::     : : |:| :| |
Db          9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSERGRWVTDLSK 63

Qy         59 T---KICIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
                 ||:  |  :| ||:: ||   |||:|:::    |  ||:::|     :||    ::
Db         64 KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWI 123

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
              |:||| | | ||||:||: | | |       |   : |:       | |:   :  : |||
Db        124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRSFAMLL 182

Qy        173 PCGIDKFRGVEFVCCP------------------------------LAEESDNVD---S 198
              ||||  : ||||||||                              : :| |: :   |
Db        183 PCGISVFSGVEFVCCPKHFKTDEIHVKKTDLPVMPAAQINSANDELVMNDEDDSNDSNYS 242

Qy        199 ADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV----------------------AE 236
              || ||| |      | |   | :::  ||:|                            ||
Db        243 KDANEDDLD------DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINAE 296

Qy        237 VEE-EEADDDEDDEDGDEVEEEAEEPY--------------------------EEATER 268
              :  || |: |:|  | | | | |  :                           |:|  :
Db        297 YDSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLKSDSSSPSSAPVAPAPEKAPVK 356

Qy        269 TTSIATTTTTTTESVEEVV----------RVPTTAASTPDAVDKYLETPGDENEHAHFQ 317
              : |: :|   :  :   |                |:|| |   | |        || ::
Db        357 SESVTSTPQLSASAAAFVAANSGNSGTGAGAPPSTAQPTS---DPYFTHFDPHYEHQSYK 413

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKA-------VIQHFQEKVESLEQE 370
              :::|||  |||:::|||::| : | : :::  || ||       :   ||  |::||:|
Db        414 VSQKRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFKQRMTARFQTSVQALEEE 473

Qy        371 AANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDR 430
              |: ||   |  || | :| |:| |:  |  ||   ||   ||   |:| :|| |||
Db        474 GNAEKHQLAAMHQQRVLAHINQRKREAMTCYIQALTEQPPNAHHVEKCLQKLLRALHKDR 533

Qy        431 QHTLKHFEH-VRMVDP---KKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI--- 483
              | | |: | :    |   : || | : :  | |   :|||:::|   | :: :|
Db        534 AHALAHYRHLLNSGGPGGLEAAASERPRTLERLIDIDRAVNQSMTMLKRYPELSAKIAQL 593

Qy        484 ----------QDEV---------------------------------------------- 487
                       :|::
Db        594 MNDYILALRSKDDIPGSSLGMSEEAEAGILDKYRVEIERKVAEKERLRLAEKQRKEQRAA 653

Qy        488 ------DELLQKEQNYSDDVLANMISE----------------------PRISYGNDAL 518
                   :| |: |    ||:| : ::|                        |   | ||
Db        654 EREKLREEKLRLEAKKVDDMLKSQVAFQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAA 713

Qy        519 M-----PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADR 573
              :     |:|  ||:          |  | | :    :|  :| :     | |     | |
Db        714 LVTAANPNLETTKS---------EKDLSDTE----YGEATVSSTKVQTVLPTVDDDAVQR 760

Qy        574 GLITRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---G 625
              :    :          ::  : : : :|   ::: |::  |     ||:   : |
Db        761 AVEDVAAA---------VAHQEAEPQVQHFMTHDLGHRESSFSLRREFAQHAHAAKEGRN 811

Qy        626 AIIGLMVGGVVIATVIVITLVMLKKKQYTSIH-HGVVEVDAAVTP------EERHLSKMQ 678
              |   |: :   : : : : | :   | |  | :|||  ||       ||: :  ||
Db        812 VYFTLSFAGIALMAAVFVGVAVAKWRTSRSPHAQGFIEVDQNVTTHHPIVREEKIVPNMQ 871

Qy        679 QNGYENPTYKFFE 691
              ||||||||||:||
Db        872 INGYENPTYKYFE 884


RESULT 15
A4_BOVIN
```

```
ID   A4_BOVIN       STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     56       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             8.0%;  Score 292;  DB 1;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-09;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        591 ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 649
              |||||||||||:||||||||||||||||||||||| ||||:|||||||:||||||.|||
Db          1 ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 59


Search completed: October  2, 2003, 13:59:35
Job time : 15 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:24 ; Search time 39 Seconds
(without alignments)
4611.863 Million cell updates/sec

Title: US-09-806-194-16
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3573	97.9	695	11	Q60496	Q60496 cavia sp. p
2	3540	97.0	695	11	P97487	P97487 mus musculu
3	3535.5	96.8	770	6	Q9TU10	Q9tu10 sus scrofa
4	3428	93.9	695	13	Q9DGJ8	Q9dgj8 gallus gall
5	3387	92.8	751	13	Q9DGJ7	Q9dgj7 gallus gall
6	3214	88.0	693	13	Q98SG0	Q98sg0 xenopus lae
7	3190	87.4	695	13	Q98SF9	Q98sf9 xenopus lae
8	3103	85.0	747	13	Q91963	Q91963 xenopus. ap
9	2964.5	81.2	699	13	O57394	O57394 narke japon
10	2767.5	75.8	569	13	Q9PVL1	Q9pvl1 gallus gall
11	2635.5	72.2	607	11	Q99K32	Q99k32 mus musculu
12	2613	71.6	534	13	O93296	O93296 gallus gall
13	2573	70.5	780	13	O73683	O73683 tetraodon f
14	2529	69.3	738	13	Q90W28	Q90w28 brachydanio
15	2487.5	68.1	694	13	Q8UUR9	Q8uur9 brachydanio
16	2448.5	67.1	737	13	O93279	O93279 fugu rubrip
17	2339	64.1	612	13	Q9I9E7	Q9i9e7 brachydanio
18	1928	52.8	384	11	Q8BPC7	Q8bpc7 mus musculu
19	1762	48.3	695	4	Q13861	Q13861 homo sapien
20	1749.5	47.9	669	4	Q14662	Q14662 homo sapien
21	1740	47.7	695	11	Q64348	Q64348 mus musculu
22	1708	46.8	763	11	Q61482	Q61482 mus musculu
23	1704	46.7	751	11	Q60709	Q60709 mus musculu
24	1655	45.3	472	13	Q8UUS0	Q8uus0 brachydanio
25	1350.5	37.0	357	13	Q8UUI8	Q8uui8 brachydanio
26	1301.5	35.6	522	4	Q9BT36	Q9bt36 homo sapien
27	1090	29.9	218	11	Q8BPV5	Q8bpv5 mus musculu
28	1048.5	28.7	523	4	Q14594	Q14594 homo sapien
29	771	21.1	239	13	Q8UUI7	Q8uui7 brachydanio
30	678	18.6	136	6	P79307	P79307 sus scrofa
31	577	15.8	113	13	Q8JH58	Q8jh58 chelydra se
32	561	15.4	182	11	Q9CYS4	Q9cys4 mus musculu
33	478	13.1	97	6	Q28673	Q28673 oryctolagus
34	393.5	10.8	82	4	Q16019	Q16019 homo sapien
35	389.5	10.7	82	4	Q16014	Q16014 homo sapien
36	387.5	10.6	82	4	Q16020	Q16020 homo sapien
37	376	10.3	79	11	O35463	O35463 cricetulus
38	358.5	9.8	160	11	Q9QZ78	Q9qz78 cavia sp. p
39	335	9.2	208	11	Q8R0R7	Q8r0r7 mus musculu
40	239	6.5	49	6	O97917	O97917 bos taurus
41	196.5	5.4	727	5	Q95TG7	Q95tg7 drosophila
42	196.5	5.4	5303	5	Q9V628	Q9v628 drosophila
43	193	5.3	785	5	Q9GQ82	Q9gq82 drosophila
44	192.5	5.3	556	5	Q95S93	Q95s93 drosophila
45	192.5	5.3	1110	13	Q91255	Q91255 petromyzon

ALIGNMENTS

RESULT 1
Q60496
ID Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative amyloid precursor protein.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 97.9%; Score 3573; DB 11; Length 695;
Best Local Similarity 97.8%; Pred. No. 2.7e-207;
Matches 680; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||  ||||||||||||||||||||||||||:||||||||||| ||||||
Db          1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWEPDPSGTK 60
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Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               ||| ||||||||| |||||||||||| |||||||||| || |||||| ||| ||||||
Db          61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 EADDDEDVEDGDEVEEEAEEPYEEATEKTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
               ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
               |||||||||||||||||||||||||||||||||||
Db         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 2
P97487
ID   P97487      PRELIMINARY;      PRT;   695 AA.
AC   P97487; P97942;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hippocampal amyloid protein.
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RA   Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 581-662 FROM N.A.
RC   STRAIN=129SV;
RA   Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA   Loring J.F., Goate A.M.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U84012; AAB41502.1; -.
DR   EMBL; U82624; AAB40919.1; -.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78414 MW;  9A5FBE2ED261236E CRC64;

  Query Match             97.0%;  Score 3540;  DB 11;  Length 695;
  Best Local Similarity   97.3%;  Pred. No. 2.6e-205;
  Matches  676;  Conservative    5;  Mismatches   14;  Indels    0;  Gaps    0;

Qy           1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
               ||| |||||||||| |||||||||||||||||||||||||||:||||||||,||:||||||
Db           1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
               |||||||||||||||:|||||||||||||||||||||||||||| ||||||||||||||:|||
Db         181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
               ||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESVEEVVRVPTTAASTPDAA 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               |||||||||||||||||||||||||||||||||||||||||||||:|||||| ||||||||
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
               |||:|||||||||||'||||||||||||||||||||||||||||||||||||||||||||||
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
               ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
               |:|:|| ||||||||'||||-||||||||||||||||||||||||||||||||||||||||
Db         601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
               |||||||||||||||||||||||||||||||||||
Db         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 3
Q9TUI0
ID   Q9TUI0      PRELIMINARY;      PRT;   770 AA.
AC   Q9TUI0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Amyloid precursor protein.
OS   Sus scrofa (Pig).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid Precursor Protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB032550; BAA84580.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   770 AA;  86961 MW;  5F7A1DCB2BC0583E CRC64;

  Query Match             96.8%;  Score 3585.5;  DB 6;  Length 770;
  Best Local Similarity   88.4%;  Pred. No. 5.6e-205;
  Matches  681;  Conservative    8;  Mismatches    6;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWDSDPSGTK 60
              |||||:|||||||||||||:|||||||.|||| :.||||:|||| |||:|:||  ||
Db          1 MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWFSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||| ||||| ||| ||| |  |||.||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||| ||||||||||||||.|:|||||'|||||.|||||.|||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||.|||||:|.|||||:|||||||||| |'||||:|||| ||||||:|||'
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              ||:|||||||||||||||||||||||||||||||| ||||:|||||
Db        241 EAEDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRFVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLLKTTQEHLPQD 360

Qy        289 ---VPTIAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||||||||||||||||||||||||||||||||||||||||.||||.|||:|||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTIVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||:|||||:||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770


RESULT 4
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             93.9%;  Score 3428;  DB 13;  Length 695;
  Best Local Similarity   94.0%;  Pred. No. 1.5e-198;
  Matches  655;  Conservative   17;  Mismatches   21;  Indels    4;  Gaps    3;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||  ||||||| |.|||||||||||||:|||||||||||:|||||||
Db          1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||| |||||||||||||||||||||||||||||||| |||  ||| |:|||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||| |||||||||||||||||||:|||| ||||||||||||||||||||
Db        121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238
              ||||:|||||||||:|||||:|||||||||| |||||:|||||    |:||:  ||
Db        181 GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVE 240

Qy        239 EEEADDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
              :|:|||| ||:|||: || || ||||||||||||||||||||||||||||||||||||||
Db        241 DEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298

Qy        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358

Qy        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM 418
              ||||||||||||||||||||||||||||||||||||:|||||||| ||||||||||
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Db        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNM 418

Qy        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPA 478

Qy        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEF 538

Qy        539 SLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 SLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDA 598

Qy        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658

Qy        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||| ||||| ||||||||||
Db        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 5
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match           92.8%;  Score 3387;  DB 13;  Length 751;
  Best Local Similarity  86.9%;  Pred. No. 4.9e-196;
  Matches  654;  Conservative   18;  Mismatches   21;  Indels   60;  Gaps    4;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||  |||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||| |||| ||| ||| |||||.|||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCNGHPHIVVPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238
              |||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        181 GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVE 240

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              |||||||| |||||||| || || ||||||||||||||||||||||||||
Db        241 DEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETG 298

Qy        289 ----------------------------------------------VPTTAASTPDAVDK 302
                                                           ||||||||||||||
Db        299 PCRAMISRWYFDVAEGKCAPFFYGGCGGNRNNFDSEEYCMAVCGSVLPTTAASTPDAVDK 358

Qy        303 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 418

Qy        363 KVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKY 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 KVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKY 478

Qy        423 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEE 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEE 538

Qy        483 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDD 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEFSLDD 598

Qy        543 LQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH 602
              ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 LQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDAEFRH 658

Qy        603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 718

Qy        663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||
Db        719 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751


RESULT 6
Q98SG0
ID   Q98SG0      PRELIMINARY;      PRT;   693 AA.
AC   Q98SG0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein A.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298150; CAC37193.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
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DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   693 AA;  78568 MW;  CAF1DF655C1AB653 CRC64;

  Query Match             88.0%;  Score 3214;  DB 13;  Length 693;
  Best Local Similarity   87.8%;  Pred. No. 1.2e-185;
  Matches  612;  Conservative   36;  Mismatches   43;  Indels    6;  Gaps    4;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPHITLLVLTV-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFR 179

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVE 238
Db        180 GVEFVCCPSAEESESFDSADA-EDDSDAWWGGADADYVDRSDDKAVEAQPDEREEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
Db        239 EEETDDDED--DGDEAEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRVPATAASTPD 296

Qy        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358
Db        297 AVDKYLENPNDENEHDRFLKAKERLEGKHRERMSEVMKEWEEAERQAKNLPKADKKAVIQ 356

Qy        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM 418
Db        357 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNM 416

Qy        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478
Db        417 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPA 476

Qy        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF 538
Db        477 VAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEF 536

Qy        539 SLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA 598
Db        537 NIEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDS 596

Qy        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658
Db        597 EYRHDTAYEVHHQKLVFFAEEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHH 656

Qy        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db        657 GVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 693

RESULT 7
Q98SF9
ID   Q98SF9      PRELIMINARY;      PRT;   695 AA.
AC   Q98SF9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein B.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298151; CAC37194.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   695 AA;  78803 MW;  DC14EB02AFB0204A CRC64;

  Query Match             87.4%;  Score 3190;  DB 13;  Length 695;
  Best Local Similarity   87.2%;  Pred. No. 3.3e-184;
  Matches  609;  Conservative   39;  Mismatches   44;  Indels    6;  Gaps    5;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR 179

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAEVE 238
Db        180 GVEFVCCPTAEESESFDSADA-EDDSDVWWGGADADYVDRSDDKAVEAQPEEEEEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR-VPTTAASTP 297
Db        239 EEEADDD-DEDDGDETEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRAVPATAVSTP 297

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
Db        298 DAVDKYLENPNDENEHDRFLKAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVI 357

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
Db        358 QHFQEKVESLEQEAANERQQLVETHMARVEATLNDRRRIALENYITALQADPPRPRHVFN 417

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
Db        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVP 477

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE 537
Db        478 AVAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGE 537

Qy        538 FSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMD 597
Db        538 FNVEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKREEISEVKMD 597

Qy        598 AEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH 657
Db        598 SEYRHDAAYEVHHQKLVFFADEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIH 657

Qy        658 HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db        658 HGVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 695

RESULT 8
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Q91963
ID   Q91963      PRELIMINARY;      PRT;   747 AA.
AC   Q91963;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   APP747.
GN   APP747.
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93129227; PubMed=1282805;
RA   Okado H., Okamoto H.;
RT   "A Xenopus homologue of the human beta-amyloid precursor protein:
RT   developmental regulation of its gene expression.";
RL   Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR   EMBL; S52417; AAB24853.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   747 AA;  84893 MW;  A75E81885681D948 CRC64;

  Query Match             85.0%;  Score 3103;  DB 13;  Length 747;
  Best Local Similarity   81.0%;  Pred. No. 6.4e-179;
  Matches  598;  Conservative   35;  Mismatches   41;  Indels   64;  Gaps    5;

Qy         17 ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQE 75
Db         15 ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE 71

Qy         76 VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF 135
Db         72 VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF 131

Qy        136 LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN 195
Db        132 LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEESES 191

Qy        196 VDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDEDDEDGDE 253
Db        192 FDSADAAEDDCDVWWGGADADYVDRSDDKAVEAQFDEEEEVVEVEEEETDDDED--DGDE 249

Qy        254 VEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------------------- 288
Db        250 AEEEPEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYYDVTE 309

Qy        289 -----------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQ 317
Db        310 SKCAQFIYGGCGGNRNNFESDDYCMAVCGSVIPATAASTPDAVDKYLENPNDENEHDRFL 369

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQ 377
Db        370 KAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ 429

Qy        378 LVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 437
Db        430 LVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 489

Qy        438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNY 497
Db        490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAVAEEIQDEVDELPQKEQNY 549

Qy        498 SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAN 557
Db        550 SDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPWHSFGVDSVPAN 609

Qy        558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA 617
Db        610 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669

Qy        618 EDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKM 677
Db        670 EEVGSNKGAIIGLMVGGVVIAIVIVITLVMLKKKQYTTIHHGVVEVDAAVTPEERHLTKM 729

Qy        678 QQNGYENPTYKFFEQMQN 695
Db        730 QQNGYENPTYKFFEQMQN 747


RESULT 9
O57394
ID   O57394      PRELIMINARY;      PRT;   699 AA.
AC   O57394;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   EL amyloid precursor protein 699.
GN   EL APP699.
OS   Narke japonica (Electric ray).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Torpediniformes; Narcinoidei; Narkidae; Narke.
OX   NCBI_TaxID=62965;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Electric lobe;
RX   MEDLINE=98129705; PubMed=9461486;
RA   Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA   Suzuki T.;
RT   "cDNA isolation of Alzheimer's amyloid precursor protein from
RT   cholinergic nerve terminals of the electric organ of the electric
RT   ray.";
RL   Biochem. J. 330:29-33(1998).
DR   EMBL; AB005544; BAA24230.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   699 AA;  78879 MW;  952915C309D50E5C CRC64;

  Query Match             81.2%;  Score 2964.5;  DB 13;  Length 699;
  Best Local Similarity   80.8%;  Pred. No. 1.3e-170;
  Matches  569;  Conservative   58;  Mismatches   58;  Indels   19;  Gaps    8;

Qy          2 LPG-LALLLLAAWTA-------RALEVPTDGNAGLL-AEPQIAMFCGRLNMHMNVQNGKW 52
Db          5 LPGRLGMLLLAAAAALVLAPLCRALEVPTDGGAGLLAAEPQIAMFCGKLNMHVNVQTGKW 64

Qy         53 DSDPSGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFV 112
Db         65 VSDPSGTNTCFGTKEGILRYCQEVYPDLQITNVVEANQPITIQNWCKKGRKQCKGHPHIV 124

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
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Db        125 VPYRCLVGEFVSDALLVPDKCKFLHREKMDTCESHLYWHTVAKETCGDKIMNLHDYGMLL 184

Qy        173 PCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEE 232

Db        185 PCGIDEFRGVEFVCCPIPEENDKIDS-DMDEEDSDVWWGGDDADYADGG-DKTV----EE 238

Qy        233 EVAEVEEEEADDDEDDEDGDEVEEE-AEEPYEEATERTTSIATTTTTTTESVEEVVRVPT 291

Db        239 KPIEEEEEEDESDIDDEDDDDLDDEVVEDQYEDPTEHTTS---STTTTTEAIEEVVRVPT 295

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351

Db        296 TAASTPDAVDKYLETPGDENEHAYFQKAKERLEAKHRERMSKIMREWEEAERQAKNLPKA 355

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411

Db        356 DKKAVIQRFQEMVESLEQEAASERQQLVETHMARVEAMLNDRRRIALENYLAALQADPPR 415

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471

Db        416 PRHVLNALKKYSRAEQKDRQHTLKHFDHVRAVDPEKAAQIKSQVMTHLHVIDERMNQSLS 475

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531

Db        476 LLYKVPSVAEEIQDEVDELLQRERSYMDDMMANSVSDTRISYGNDALVPSLSETKTTIEL 535

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI 591

Db        536 LPDDGEFILDDLQPPHPFVIESIPANTENEVEPVDARPAPDRGLTTRPGSGLTGIKTEEI 595

Qy        592 SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 651

Db        596 AELKMETEFQQDSGYEVHHQKLVFFPKDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 655

Qy        652 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Db        656 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 699
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RESULT 10
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             75.8%;  Score 2767.5;  DB 13;  Length 569;
  Best Local Similarity   93.5%;  Pred. No. 7.6e-159;
  Matches  535;  Conservative   14;  Mismatches   18;  Indels    5;  Gaps    4;

Qy        126 ALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFV 185

Db          1 ALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLSCGIDKFRGVEFV 60

Qy        186 CCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVEEEEAD 243

Db         61 CCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVEDEDAD 120

Qy        244 DDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAVDKY 303

Db        121 DD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDVVDKY 178

Qy        304 LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEK 363

Db        179 LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEK 238

Qy        364 VESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYV 423

Db        239 VESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKYV 298

Qy        424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI 483

Db        299 RAEQKDRQHTLKHFEHVRMVDPKKAVQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEEI 358

Qy        484 QDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDL 543

Db        359 QDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPTLTETKTTVELLPVVGEFSLDDL 418

Qy        544 QPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHD 603

Db        419 QPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDAEFRHD 478

Qy        604 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEV 663

Db        479 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIANVIVITLVMLKKKQYTSIHHGVVEV 538

Qy        664 DAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Db        539 DAAVTP-ERHLSKMQQNGYENPTYKFFEQMQN 569
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RESULT 11
Q99K32
ID   Q99K32      PRELIMINARY;      PRT;   607 AA.
AC   Q99K32;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical 68.4 kDa protein (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005490; AAH05490.1; -.
DR   HSSP; P05067; 1AAP.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
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DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
FT   NON_TER      1      1
SQ   SEQUENCE   607 AA;  68391 MW;  BF802214CBA7D172 CRC64;

  Query Match             72.2%;  Score 2635.5;  DB 11;  Length 607;
  Best Local Similarity   85.7%;  Pred. No. 7.5e-152;
  Matches  520;  Conservative    4;  Mismatches    8;  Indels   75;  Gaps    1;

Qy        164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSED 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db          1 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGED 60

Qy        224 KVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESV 283
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVVEVAEEEEVADVEEEEADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESV 120

Qy        284 EEVVR---------------------------------------------------------- 288
              |||||
Db        121 EEVVRFVCSEQAETGPCRAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGS 180

Qy        289 ----------------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHR 328
                                   :|.||||:|||||.|||||.|||| |||||. |||||.|
Db        181 VSTQSLLKTTSEPLPQDPDKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHR 240

Qy        329 ERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEA 388
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEA 300

Qy        389 MLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKA 448
              ||||||||||||||||||.||||  |||||||||||||||||||||||||||||||||||
Db        301 MLNDRRRLALENYITALQAVPPRPRHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKA 360

Qy        449 AQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISE 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISE 420

Qy        509 PRISYGNDALMPSLIETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDAR 568
              |||||||||:|||||||||||||||||||||||||:|||| || |||:|||.|||||||||
Db        421 PRISYGNDALMPSLIETKTTVELLPVNGEFSLDDLQPWHPFGVDSVPANIENEVEPVDAR 480

Qy        569 PAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 628
              |||||||||||||||||||||||||||||||||||| |||||:| ||||||||||||||||
Db        481 PAADRGLTTRPGSGLTNIKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAII 540

Qy        629 GLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYK 688
              |||||||||||||||||||||||||||||||||||||:|||||:|||||| ||| |||||,
Db        541 GLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYK 600

Qy        689 FFEQMQN 695
              |||||||
Db        601 FFEQMQN 607


RESULT 12
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER      1      1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             71.6%;  Score 2613;  DB 13;  Length 534;
  Best Local Similarity   94.8%;  Pred. No. 1.4e-149;
  Matches  506;  Conservative   13;  Mismatches   11;  Indels    4;  Gaps    3;

Qy        164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSED 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDD 62

Qy        224 KVVE--VAEEEEVAEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTE 281
              ||||    |:||:  ||:|:|||| ||:|||: || |. |||||||||||||||||||
Db         63 KVVEEQPEEDEELTVVEDEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTE 120

Qy        282 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 180

Qy        342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENY 401
              ||||||||||||||||||||||||||||||||||||||||||||||||:|||||:|||||
Db        181 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENY 240

Qy        402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ITALQTVPPRPRHVFNMLKKYVRAEQKDRQHILKHFEHVRMVDPKKAAQIRSQVMTHLRV 300

Qy        462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 521
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IYERMNQSLSFLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 360

Qy        522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGS 581
              |||||||||||||:|||||||||||| || ||||||||||||||||||||||||||||||
Db        361 LTETKTTVELLPVDGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGS 420

Qy        582 GLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 641
              :|||:||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GLTNVKTEEVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 480

Qy        642 VITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 534


RESULT 13
O73683
ID   O73683      PRELIMINARY;      PRT;   780 AA.
AC   O73683;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Tetraodon fluviatilis (Puffer fish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GIP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC       WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC       RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC       NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC       PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
CC       BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    780       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                HOMOLOG.
FT   CHAIN       682    724       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    732       POTENTIAL.
FT   DOMAIN      733    780       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      323    382       BPTI/KUNITZ INHIBITOR.
FT   SITE        769    772       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    327    378       BY SIMILARITY.
FT   DISULFID    336    361       BY SIMILARITY.
FT   CARBOHYD    560    560       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   780 AA;  88238 MW;  60071BE94520191D CRC64;

  Query Match             70.5%;  Score 2573;  DB 13;  Length 780;
  Best Local Similarity   65.4%;  Pred. No. 6.1e-147;
  Matches  513;  Conservative   71;  Mismatches   94;  Indels  106;  Gaps   10;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
              |||:|| :  | ||||| : |||||||:||||::|||:|||:|||: |:|||||:|| ||
Db          8 LLLVAAASTLAAEVPTDVSMGLLAEPQVAMFCGKINMHINVQSGKWEPDPSGTKSCIGTK 67

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
              |||||||||||||||||||||||||:||||||:||||||::| | |:|||||||||||||
Db         68 EGILQYCQEVYPELQITNVVEANQPVSIQNWCKKGRKQCRSHMHIVVPYRCLVGEFVSDA 127

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
              |||||||||||||||: ||:||||||||||:| ::: ||||||||:||||:|||||||||
Db        128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVEFVC 187

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS----------EDKVVEVAEEE 232
              || ||   ::|| : : |||||||||||| |||:| |               |||  ||
Db        188 CP-AEAERDMDSTEKDADDSDVWWGGADNDYSDNSMVREPEPAEQQEETRPSVVEEEEEG 246

Qy        233 EVAEVEEEE----------------ADDDEDDEDGDEVEEEAEEPYEEATERTISIA 273
              |:|: ::||                |||:|:::|| ||::   |    :| | ||::|
Db        247 EVAQEDDEEEEEVLDTDQDGDGEEDHEAADDEEEEEDVDEIDAFGESDDVDADEPTINVA 306

Qy        274 ---TTTTTTTESVEEVVR---------------------------------------- 288
                 |||||||||||:|||
Db        307 MTTTTTTTTTESVEEVVRMFCWAHADTGPCTASMPSWYFDAVDGRTMYELMYGGCGGNMN 366

Qy        289 --------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQ 333
                           |||   |:||||| ||||| |||||||:||||| ||||||||||
Db        367 NFESEEYCLSVCSSVVPTDMPSSPDAVDHYLETPADENEHAHFQKAKESLEAKHRERMSQ 426

Qy        334 VMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDR 393
              |||||||||||||||||:|||| ||| |||||:||||||:|||||||||||||||:||||
Db        427 VMREWEEAERQAKNLPRADKKIVIQRFQEKVEALEQEAASERQQLVETHMARVEALLNDR 486

Qy        394 RRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRS 453
              |||||||||:|||| |||||||||::||||||||||||||||||||||||||||||||||
Db        487 RRLALENYLTALQQDPPRPRHVFSLLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRP 546

Qy        454 QVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
              ||:|||||| |||||||| ||| '| ||::|||:| ||||:||      |||: :: |:||
Db        547 QVLTHLRVIEERMNQSLGLLYKVPGVADDIQDQV-ELLQREQAEMAQQLANLQTDVRVSY 605

Qy        514 GNDALMPSLTETKTTVELLPVNGEFSLDDLQPWH--SFGADSVPANTENEVEPVDARPAA 571
              |||||||          :|||   | :|  :   |  ||       ||||:|||||:||
Db        606 GNDALMPDQELGDGQADLLP--QEDTLGGVGFVHPESFN----QLNTENQVEPVDSRPTF 659

Qy        572 DRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLM 631
              :||: |||   :|    | : |::|: | :  : ||||||||||||||||||:|||||||
Db        660 ERGVPTRP---VTGKSMEAVPELRMETEDRQSTEYEVHHQKLVFFAEDVGSNKGAIIGLM 716

Qy        632 VGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
              |||||||||'|||||||:|||,||||||::|||||||||||||||||:|||||||||||
Db        717 VGGVVIATVIVITLVMLRKKQYTSIHHGIIEVDAAVIPEERHLSKMQQNGYENPTYKFFE 776

Qy        692 QMQN 695
              ||||
Db        777 QMQN 780


RESULT 14
Q90W28
ID   Q90W28      PRELIMINARY;      PRT;   738 AA.
AC   Q90W28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid precursor protein.
GN   APPA OR APP.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Expression analysis of zebrafish app.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389401; AAK64495.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
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DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   738 AA;  83577 MW;  AF480F6D308FD298 CRC64;

  Query Match             69.3%;  Score 2529;  DB 13;  Length 738;
  Best Local Similarity   66.4%;  Pred. No. 2.5e-144;
  Matches  501;  Conservative   79;  Mismatches   90;  Indels   84;  Gaps   14;

Qy          5 LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCID 64
Db          6 LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPDPSGSKSCIG 65

Qy         65 TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVS 124
Db         66 NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS 125

Qy        125 DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF 184
Db        126 DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF 185

Qy        185 VCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADD 244
Db        186 VCCP-ADAGKESESAAVEEDDSDVWWGGAFADYTENSMTR--DAAAEPAVLE-DDEDADE 241

Qy        245 DED-DEDGD-----EVEEEAEEPYEEATERTT-STATTTTTTTESVEEVVR--------- 288
Db        242 EEDEDQDGDGDRDEKIEEEEEE--EERTQSTSAALTSTTTTTTTESVEEVVREVCFASAET 299

Qy        289 ---------------------------------------------VPTTAASTPDAVD 301
Db        300 GPCRAMLSRWYYVREERRCAPFIYGGCGGNRNNFESEEYCLSVCSGVLPTPSSSPPDAVD 359

Qy        302 KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQ 361
Db        360 RYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAKSLPRNDKKAVIQHFQ 419

Qy        362 EKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKK 421
Db        420 EKVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQADPPRPRHVFSLLKK 479

Qy        422 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAE 481
Db        480 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVAD 539

Qy        482 EIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLD 541
Db        540 DIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFG 595

Qy        542 DLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFR 601
Db        596 FIHP-ESFN----QPNTHNQVEPVDARPVPDLDLATRPVSGL---KPDDIPELRMEAHER 647

Qy        602 HDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVV 661
Db        648 HS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIVITLVMLRKKQYTSIHHGII 704

Qy        662 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db        705 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 738
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RESULT 15
Q8UUR9

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ID   Q8UUR9      PRELIMINARY;      PRT;   694 AA.
AC   Q8UUR9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Putative membrane protein.
GN   APPB.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11862463;
RA   Musa A., Lehrach H., Russo V.E.A.;
RT   "Distinct expression patterns of two zebrafish homologues of the human
RT   APP gene during embryonic development.";
RL   Dev. Genes Evol. 211:563-567(2001).
DR   EMBL; AJ315639; CAC85736.1; -.
DR   ZFIN; ZDB-GENE-020220-1; appb.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   694 AA;  79228 MW;  2BC3382D411162DC CRC64;

  Query Match             68.1%;  Score 2487.5;  DB 13;  Length 694;
  Best Local Similarity   67.9%;  Pred. No. 7.5e-142;
  Matches  477;  Conservative   98;  Mismatches   97;  Indels   31;  Gaps    9;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
Db          9 LLLMLTTLSLAIEVPSDDSVGLLAEPQVAMFCGKLNMHINVQSGKWEPDPTGTKSCISTK 68

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
Db         69 EGILKYCQEVYPDLQITNVVEANQPVSIQNWCKMGRRQCRSHTHIVVPYRCLVGEFVSDA 128

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
Db        129 LLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVC 188

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS--EDKVV-----EVAEEEEVAEVEE 239
Db        189 CPMEEQKD-LDSEEQEEANSDVWWGGAETEYTDASVLKEQVTAKPDPAVTEDDEDLNNEE 247

Qy        240 EEADDDEDDEDGDEVEEEAEE-----PYEEATERTTSIA--TTTTTTTESVEEVVRVPTT 292
Db        248 EEVWDNDEDGDGEDDEDEEDDDEDIIDEQDTSEQTSNIAMTTTTTTTIESIEEVVRVPTM 307

Qy        293 AASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKAD 352
Db        308 APSPADAVDRYLEAPGDMNEHMRFQKAKESLEAKHREKMSEVMREWEEAERQAKNLPRAD 367

Qy        353 KKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRP 412
Db        368 KKTIIQRFQEKVESLEKEAAGERQQLVETHMARVEALLNDRRRQALESYLSSLQSDQPRP 427

Qy        413 RHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSL 472
Db        428 RQVLNLLKKYIRAEQKDRQHTLKHFEHVREVDPKKASQIRPFVMTHLRVIEERMNQSLGY 487

Qy        473 LYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELL 532
Db        488 LYKVPQVANDIQDQVAVLVQRDQAEVTQQLSSLQSKMRVSYGNDALMPDLPDSTTPLDNL 547

Qy        533 PVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEIS 592
Db        548 PPEQD-GLGFIHP-ESFN----QANTDNHVEPVDARPIPERGLPTRP----------EIP 591

Qy        593 EVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQ 652
Db        592 KVRLDIEERHNAGYDVRDKRLMFLAEDMGSNKGAIIGLMVGGVVIATVIVITLVMLRKKQ 651
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Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||.||||:|||||||||||||||:|||||||||||||||||| |
Db        652 YTSIHHGVIEVDAAVTPEERHLAKMQQNGYENPTYKFFEQMQN 694

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Job time : 43 secs
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GenCore version 5.1.6

CM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:09 ; Search time 38.3333 Seconds
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Title: US-09-806-194-18
Perfect score: 3651
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3651	100.0	697	21	AAY88429	Human APPSW-KK ami
2	3651	100.0	697	22	AAE10636	Human amyloid prot
3	3651	100.0	697	22	AAE06866	Human amyloid prec
4	3651	100.0	697	22	AAU06610	Human Amyloid prec
5	3651	100.0	697	22	AAU07209	Human beta-amyloid
6	3651	100.0	697	22	AAE02588	Human amyloid prec
7	3651	100.0	697	23	ABB78597	Human APP695-Sw-KK
8	3643	99.8	697	21	AAY88428	Human APP695-KK am
9	3643	99.8	697	22	AAE10635	Human amyloid prot
10	3643	99.8	697	22	AAE06865	Human amyloid prec
11	3643	99.8	697	22	AAU06609	Human Amyloid prec
12	3643	99.8	697	22	AAU07208	Human beta-amyloid
13	3643	99.8	697	22	AAE02587	Human amyloid prec
14	3643	99.8	697	23	ABB78596	Human APP695-KK pr
15	3641	99.7	695	21	AAY88435	Human APP695-sw va
16	3641	99.7	695	22	AAE10633	Human amyloid prot
17	3641	99.7	695	22	AAE06863	Human amyloid prec
18	3641	99.7	695	22	AAU06607	Human Amyloid prec
19	3641	99.7	695	22	AAU07206	Human beta-amyloid
20	3641	99.7	695	22	AAE02585	Human amyloid prec
21	3641	99.7	695	23	ABB78594	Human APP695-Sw pr
22	3638	99.6	697	21	AAY88430	Human APP695-VF-KK
23	3638	99.6	697	22	AAE10637	Human amyloid prot
24	3638	99.6	697	22	AAE06867	Human amyloid prec
25	3638	99.6	697	22	AAU06611	Human Amyloid prec
26	3638	99.6	697	22	AAU07210	Human beta-amyloid
27	3638	99.6	697	22	AAE02589	Human amyloid prec
28	3638	99.6	697	23	ABB78598	Human APP695-VF-KK
29	3636	99.6	695	18	AAW19504	APP695 mutant A-be
30	3636	99.6	695	18	AAW19490	APP695 mutant A-be
31	3633	99.5	695	9	AAP81692	Sequence of human
32	3633	99.5	695	13	AAR26338	APP695. Homo sapi
33	3633	99.5	695	19	AAY20233	Human beta-amyloid
34	3633	99.5	695	20	AAY07221	Amyloid precursor
35	3633	99.5	695	21	AAY88434	Human APP695 amino
36	3633	99.5	695	21	AAY44705	Human beta amyloid
37	3633	99.5	695	22	AAE10632	Human wild-type am
38	3633	99.5	695	22	AAE06862	Human wild-type am
39	3633	99.5	695	22	AAU06606	Human Amyloid prec
40	3633	99.5	695	22	AAE02584	Human amyloid prec
41	3633	99.5	695	23	ABG32721	Human amyloid prec
42	3633	99.5	695	23	ABB78593	Human APP695 prote
43	3633	99.5	695	23	AAG68315	Human amyloid prec
44	3633	99.5	695	24	ABB99604	Amino acid sequenc
45	3630	99.4	695	20	AAY49690	Human beta amyloid

ALIGNMENTS

RESULT 1
AAY88429
ID AAY88429 standard; Protein; 697 AA.
XX
AC AAY88429;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human APPSW-KK amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APPSW-KK.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15666.
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

```
PT   the beta secretase site to produce amyloid beta peptide -
XX
PS   Claim 133; Page 143-147; 183pp; English.
XX
CC   This sequence represents a modified version of the human amyloid
CC   precursor protein (APP) amino acid sequence. The sequence is used in an
CC   example of the method of the invention, to show that modification of APP
CC   increases beta amyloid protein processing. The invention relates to a
CC   protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC   amyloid precursor protein (APP). The protease contains a sequence
CC   encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC   separated by 100-300 amino acids. When mutated the APP gene causes an
CC   autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC   surface membrane and have a single C-terminal transmembrane domain.
CC   Proteolytic processing of APP produces the amyloid beta protein, which is
CC   possibly very important in Alzheimer's disease. The invention includes a
CC   nucleotide sequence encoding the protease, a vector containing the
CC   nucleotide sequence, and a cell line comprising the vector. Methods for
CC   screening for inhibitors of beta secretase activity are also given in the
CC   invention. The human aspartase protein and nucleotide sequences and the
CC   methods for identifying inhibitors of the protease, are useful in the
CC   treatment of and research in to Alzheimer's disease.
XX
SQ   Sequence   697 AA;

  Query Match             100.0%;  Score 3651;  DB 21;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTITESVEEVVRVPITAASIPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTITESVEEVVRVPITAASIPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 2
AAE10636
ID   AAE10636 standard; Protein; 697 AA.
XX
AC   AAE10636;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human amyloid protein precursor 695-Sw-KK (APP695-Sw-KK) isoform.
XX
KW   Human; aspartyl protease 1; Aspl; amyloid precursor protein;
KW   Alzheimer's disease; AD; dementia;  neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   APP695-Sw-KK; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 595
FT                   /note= "Wild-type Lys substituted with Asn"
FT   Misc-difference 596
FT                   /note= "Wild-type Met substituted with Leu"
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-0023315.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   N-PSDB; AAD17872.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with
PT   amyloid precursor protein processing activity and alpha-secretase
PT   activity, for identifying modulators useful in treating Alzheimer's
PT   disease -
XX
PS   Example 6; Page 117-119; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC   Aspl proteins which lack transmembrane domain or amino terminal
CC   domain or cytoplasmic domain and retains alpha-secretase activity
CC   and amyloid protein precursor (APP) processing activity. The proteins
CC   of the invention are useful for assaying hu-Aspl alpha-secretase
CC   activity, which in turn is useful for identifying modulators of
CC   hu-Aspl alpha-secretase activity, where modulators that increase
CC   hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC   disease (AD) which causes progressive dementia with consequent
CC   formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC   neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC   hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC   the substrate under acidic conditions and determining the level of
CC   hu-Aspl proteolytic activity. The present sequence is human amyloid
CC   protein precursor 695-Sw-KK (APP695-Sw-KK) isoform which is obtained
CC   by the addition of two lysine residues (KK motif) at the C-terminal
CC   of App695-Sw isoform which is generated by the Swedish mutation
CC   APP695, where Lys at position 595 is replaced with Asn and Met at
```

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CC   position 596 is replaced with Leu. APP695-Sw-KK isoform is useful
CC   for assaying the beta-secretase activity of human aspartyl protease
CC   2a (hu-Asp2a) protein.
XX
SQ   Sequence   697 AA;

  Query Match           100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 3
AAE06866
ID   AAE06866 standard; Protein; 697 AA.
XX
AC   AAE06866;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-Sw-KK (APP695-Sw-KK) isoform.
XX
KW   Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-Sw-KK;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; gene therapy; APP695-Sw-KK; mutant;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 595
FT                   /note= "Wild type Lys substituted with Asn"
FT   Misc-difference 596
FT                   /note= "Wild type Met substituted with Leu"
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00799.
XX
PR   09-MAY-2001; 2001WO-IB00799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PT   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-483072/52.
DR   N-PSDB; AAD13028.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 147-149; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting
CC   Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC   blots. The present sequence is modified human amyloid precursor
CC   protein 695-Swedish (APP695-Sw-KK) isoform. APP695-Sw-KK isoform is
CC   obtained by addition of two Lys residues (KK motif) at the C-terminal
CC   end of APP695-Sw isoform. APP695-Sw isoform is obtained by Swedish KM-NL
CC   mutation in APP695 isoform, where Lys at position 595 is replaced with
CC   Asn, Met at position 596 is replaced with Leu. APP695-Sw-KK isoform is
CC   useful for assaying the beta-secretase activity of human aspartyl
CC   protease 2a (Hu-Asp2a) protein.
XX
SQ   Sequence   697 AA;

  Query Match           100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTITTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTITTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLIETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Db        541 DDLQPWHSFGADSVPANIENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 4
AAU06610
ID   AAU06610 standard; Protein; 697 AA.
XX
AC   AAU06610;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-SW-KK.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-SW-KK; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 595..596
FT                   /note= "Wild-type Lys-Met substituted by Asn-Leu"
FT   Misc-difference 696..697
FT                   /note= "2 Extra Lys residues added compared to
FT                   wild-type APP695"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00798.
XX
PR   09-MAY-2001; 2001WO-IB00798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502549/55.
DR   N-PSDB; AAS11524.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 147-149; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp
CC   proteins and vectors expressing them, and a polypeptide (isoform of
CC   amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC   APP or its fragment containing an APP cleavage site recognizable by a
CC   mammalian beta-secretase, and further comprising two lysine residues at
CC   the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC   APP fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and
CC   amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease.
CC   APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC   is associated with increased levels of Abeta processing is useful in
CC   assays relating the Alzheimer's research. The expression vector is useful
CC   for recombinantly expressing APP. Nucleic acids that hybridise to
CC   Asp oligonucleotides are  useful as probes or primers. The probes are
CC   useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence is the human
CC   APP695 mutant, APP695-SW-KK which has 2 extra Lys residues added at
CC   the C-terminus compared to the APP695-SW mutant. The mutation alters the
CC   specificity of the APP gamma-secretase activity and increases the rate
CC   of processing of the amyloid Abeta peptide.
XX
SQ   Sequence   697 AA;

  Query Match             100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTITSIATTTITTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTITTTESVEEVVRVPTTAASTPDAV 300
```

```
Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 5
AAU07209
ID   AAU07209 standard; Protein; 697 AA.
XX
AC   AAU07209;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human beta-amyloid protein precursor, APP695-Sw-KK.
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; APP695-Sw-KK.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 595
FT                   /note= "Wild type Lys substituted by Asn"
FT   Misc-difference 596
FT                   /note= "Wild type Met substituted by Leu"
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00797.
XX
PR   09-MAY-2001; 2001WO-IB00797.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-502548/55.
DR   N-PSDB; AAS11709.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 147-149; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing
CC   an APP cleavage site recognisable by a mammalian beta-secretase, and
CC   further comprising two lysine residues at the carboxyl terminus of the
CC   amino acid sequence of the mammalian APP or APP fragment. The
CC   polypeptides are used for assaying for modulators of beta-secretase
CC   activity; identifying agents that inhibit the APP processing activity
CC   of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC   modulate the activity of Asp2; and for reducing cellular production of
CC   amyloid beta (Abeta) from APP. Agents identified by the above methods
CC   are useful for treating Alzheimer's disease; and for identifying
CC   modulators of amyloid-beta (Abeta) peptide production, for use in
CC   designing therapeutics for the treatment or prevention of Alzheimer's
CC   disease. Probes and primers derived from Asp nucleic acid sequences
CC   are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence represents the
CC   amino acid sequence of human amyloid protein precursor, APP695-Sw-KK,
CC   used in the method of the invention.
XX
SQ   Sequence   697 AA;

  Query Match             100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASIPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASIPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
```

```
Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||| |||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 6
AAE02588
ID   AAE02588 standard; Protein; 697 AA.
XX
AC   AAE02588;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-Sw-KK (APP695-Sw-KK).
XX
KW   Human; alpha-secretase; amyloid precursor protein 695-Sw-KK; therapy;
KW   APP695-Sw-KK; Alzheimer's disease; antialzheimer's.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200123533 A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26080.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M, Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   N-PSDB; AAD05746.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Example 6; Page 146-148; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human APP695-Sw-KK. This
CC   sequence contains a Sw mutation which is characterised by a KM to NL
CC   alteration at positions 595-596 and two lysine residues at the
CC   carboxyl-terminal end.
XX
SQ   Sequence   697 AA;

  Query Match           100.0%;  Score 3651;  DB 22;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 7
ABB78597
ID   ABB78597 standard; Protein; 697 AA.
XX
AC   ABB78597;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human APP695-Sw-KK protein sequence SEQ ID NO:18.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW   proteolytic; amyloid precursor protein; APP.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-0025934.
XX
PR   23-SEP-1999;   99US-155493P.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-169232P.
PR   22-SEP-2000; 2000GB-0023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ, Gurney M;
XX
DR   WPI; 2002-396337/43.
```

```
DR   N-PSDB; ABL52464.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect
PT   aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT   disease -
XX
PS   Example 6; Page 117-119; 182pp; English.
XX
CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC   proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the
CC   non-coding strand complementary to a defined 1804 nucleotide sequence
CC   (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC   Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC   domain); (3) a purified polynucleotide (III') comprising a sequence that
CC   hybridises under stringent conditions to (III) (the nucleotide sequence
CC   encodes a polypeptide further lacking a pro-peptide domain corresponding
CC   to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC   comprising (III) or (III'); and (5) a host cell (V) transformed or
CC   transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC   substrate (I) may be used as an enzyme substrate in assays to detect
CC   aspartyl protease activity, (II) and therefore diagnose diseases
CC   associated with aberrant hu-Asp1 expression and activity such as
CC   Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC   hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC   sequence represents human amyloid precursor protein APP695-Sw-KK, which
CC   is given in an example from the present invention.
XX
SQ   Sequence   697 AA;

  Query Match             100.0%;  Score 3651;  DB 23;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-256;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 8
AAY88428
ID   AAY88428 standard; Protein; 697 AA.
XX
AC   AAY88428;
XX
DT   03-AUG-2000  (first entry)
XX
DE   Human APP696-KK amino acid sequence.
XX
KW   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW   Alzheimer's disease; beta secretase site; APP696-KK.
XX
OS   Homo sapiens.
XX
PN   WO200017369-A2.
XX
PD   30-MAR-2000.
XX
PF   23-SEP-1999;   99WO-US20881.
XX
PR   24-SEP-1998;   98US-0101594.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2000-303209/26.
DR   N-PSDB; AAA15665.
XX
PT   New enzyme designated human aspartase useful in research into
PT   Alzheimer's Disease is capable of cleaving amyloid protein precursor at
PT   the beta secretase site to produce amyloid beta peptide -
XX
PS   Claim 132; Page 137-141; 183pp; English.
XX
CC   This sequence represents a modified version of the human amyloid
CC   precursor protein (APP) amino acid sequence. The sequence is used in an
CC   example of the method of the invention, to show that modification of APP
CC   increases beta amyloid protein processing. The invention relates to a
CC   protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC   amyloid precursor protein (APP). The protease contains a sequence
CC   encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC   separated by 100-300 amino acids. When mutated the APP gene causes an
CC   autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC   surface membrane and have a single C-terminal transmembrane domain.
CC   Proteolytic processing of APP produces the amyloid beta protein, which is
CC   possibly very important in Alzheimer's disease. The invention includes a
CC   nucleotide sequence encoding the protease, a vector containing the
CC   nucleotide sequence, and a cell line comprising the vector. Methods for
CC   screening for inhibitors of beta secretase activity are also given in the
CC   invention. The human aspartase protein and nucleotide sequences and the
CC   methods for identifying inhibitors of the protease, are useful in the
CC   treatment of and research in to Alzheimer's disease.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3643;  DB 21;  Length 697;
```

```
  Best Local Similarity   99.7%;  Pred. No. 5.3e-256;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
AAE10635
ID   AAE10635 standard; Protein; 697 AA.
XX
AC   AAE10635;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human amyloid protein precursor 695-KK (APP695-KK) isoform.
XX
KW   Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-KK;
KW   Alzheimer's disease; AD; dementia;  neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-0023315.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   N-PSDB; AAD17871.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with
PT   amyloid precursor protein processing activity and alpha-secretase
PT   activity, for identifying modulators useful in treating Alzheimer's
PT   disease -
XX
PS   Example 6; Page 114-116; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC   Aspl proteins which lack transmembrane domain or amino terminal
CC   domain or cytoplasmic domain and retains alpha-secretase activity
CC   and amyloid protein precursor (APP) processing activity. The proteins
CC   of the invention are useful for assaying hu-Aspl alpha-secretase
CC   activity, which in turn is useful for identifying modulators of
CC   hu-Aspl alpha-secretase activity, where modulators that increase
CC   hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC   disease (AD) which causes progressive dementia with consequent
CC   formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC   neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC   hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC   the substrate under acidic conditions and determining the level of
CC   hu-Aspl proteolytic activity. The present sequence is human amyloid
CC   protein precursor 695-KK (APP695-KK) isoform which is obtained by
CC   the addition of two Lys residues (KK motif) at the C-terminus of
CC   APP695 protein.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3643;  DB 22;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 5.3e-256;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 10
AAE06865
ID   AAE06865 standard; Protein; 697 AA.
XX
AC   AAE06865;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-KK (APP695-KK) isoform.
XX
KW   Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; gene therapy; APP695-KK; mutant;
KW   mutein.
XX
OS   Homo sapiens.
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00799.
XX
PR   09-MAY-2001; 2001WO-IB00799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-483072/52.
DR   N-PSDB; AAD13027.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting
CC   Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC   blots. The present sequence is modified human amyloid precursor
CC   protein 695-KK (APP695-KK) isoform. APP695-KK isoform is obtained by
CC   addition of two Lys residues (KK motif) at the C-terminal end of APP695
CC   isoform.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3643;  DB 22;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 5.3e-256;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

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RESULT 11
AAU06609
ID   AAU06609 standard; Protein; 697 AA.
XX
AC   AAU06609;
```

```
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-KK.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-KK; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 696..697
FT                   /note= "2 Extra Lys residues added compared to
FT                   wild-type APP695"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00798.
XX
PR   09-MAY-2001; 2001WO-IB00798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-502549/55.
DR   N-PSDB; AAS11523.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp
CC   proteins and vectors expressing them, and a polypeptide (isoform of
CC   amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC   APP or its fragment containing an APP cleavage site recognizable by a
CC   mammalian beta-secretase, and further comprising two lysine residues at
CC   the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC   APP fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and
CC   amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease.
CC   APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC   is associated with increased levels of Abeta processing is useful in
CC   assays relating the Alzheimer's research. The expression vector is useful
CC   for recombinantly expressing APP. Nucleic acids that hybridise to
CC   Asp oligonucleotides are useful as probes or primers. The probes are
CC   useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence is the human
CC   APP695 mutant, APP695-KK which has 2 extra Lys residues added at
CC   the C-terminus compared to the wild-type APP695. The mutation alters the
CC   specificity of the APP gamma-secretase activity and increases the rate
CC   of processing of the amyloid Abeta peptide.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3643;  DB 22;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 5.3e-256;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASIPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 12
AAU07208
ID   AAU07208 standard; Protein; 697 AA.
XX
AC   AAU07208;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human beta-amyloid protein precursor, APP695-KK.
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; APP695-KK.
XX
OS   Homo sapiens.
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00797.
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XX
PR   09-MAY-2001; 2001WO-IB00797.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502548/55.
DR   N-PSDB; AAS11708.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity  -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing
CC   an APP cleavage site recognisable by a mammalian beta-secretase, and
CC   further comprising two lysine residues at the carboxyl terminus of the
CC   amino acid sequence of the mammalian APP or APP fragment. The
CC   polypeptides are used for assaying for modulators of beta-secretase
CC   activity; identifying agents that inhibit the APP processing activity
CC   of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC   modulate the activity of Asp2; and for reducing cellular production of
CC   amyloid beta (Abeta) from APP. Agents identified by the above methods
CC   are useful for treating Alzheimer's disease; and for identifying
CC   modulators of amyloid-beta (Abeta) peptide production, for use in
CC   designing therapeutics for the treatment or prevention of Alzheimer's
CC   disease. Probes and primers derived from Asp nucleic acid sequences
CC   are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence represents the
CC   amino acid sequence of human amyloid protein precursor, APP695-KK,
CC   used in the method of the invention.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3643;  DB 22;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 5.3e-256;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  :||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 13
AAE02587
ID   AAE02587 standard; Protein; 697 AA.
XX
AC   AAE02587;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-KK (APP695-KK).
XX
KW   Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
KW   therapy; Alzheimer's disease; antialzheimer's.
XX
OS   Homo sapiens.
CS   Synthetic.
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26080.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   N-PSDB; AAD06745.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Example 6; Page 143-145; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human APP695-KK. This
CC   sequence contains two carboxy-terminal lysine residues.
XX
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SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3643;  DB 22;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 5.3e-256;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 14
ABB78596
ID   ABB78596 standard; Protein; 697 AA.
XX
AC   ABB78596;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human APP695-KK protein sequence SEQ ID NO:16.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW   proteolytic; amyloid precursor protein; APP.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-0025934.
XX
PR   23-SEP-1999;   99US-155493P.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-169232P.
PR   22-SEP-2000; 2000GB-0023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2002-396337/43.
DR   N-PSDB; ABL52463.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect
PT   aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT   disease -
XX
PS   Example 6; Page 114-116; 182pp; English.
XX
CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 6 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC   proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the
CC   non-coding strand complementary to a defined 1804 nucleotide sequence
CC   (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC   Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC   domain); (3) a purified polynucleotide (III') comprising a sequence that
CC   hybridises under stringent conditions to (III) (the nucleotide sequence
CC   encodes a polypeptide further lacking a pro-peptide domain corresponding
CC   to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC   comprising (III) or (III'); and (5) a host cell (V) transformed or
CC   transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC   substrate (I) may be used as an enzyme substrate in assays to detect
CC   aspartyl protease activity, (II) and therefore diagnose diseases
CC   associated with aberrant hu-Asp1 expression and activity such as
CC   Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC   hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC   sequence represents human amyloid precursor protein APP695-KK, which is
CC   given in an example from the present invention.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3643;  DB 23;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 5.3e-256;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 15
AAY88435
ID AAY88435 standard; Protein; 695 AA.
XX
AC AAY88435;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human APP695-sw variant amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15672.
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at
PT the beta secretase site to produce amyloid beta peptide -
XX
PS Example 6; Page 125-129; 183pp; English.
XX
CC This sequence represents a human amyloid precursor protein 695 (APP695)
CC variant amino acid sequence. The sequence is used in an example of the
CC invention, showing that modification of APP can increase beta amyloid
CC peptide processing. The invention relates to a protease (e.g. Asp2)
CC capable of cleaving the beta secretase site of amyloid precursor protein
CC (APP). The protease contains a sequence encoding the amino acid sequence
CC DTG and a sequence encoding DSG or DTG separated by 100-300 amino acids.
CC When mutated the APP gene causes an autosomal dominant form of
CC Alzheimer's disease. APP localises to the cell surface membrane and have
CC a single C-terminal transmembrane domain. Proteolytic processing of APP
CC produces the amyloid beta protein, which is possibly very important in
CC Alzheimer's disease. The invention includes a nucleotide sequence
CC encoding the protease, a vector containing the nucleotide sequence, and a
CC cell line comprising the vector. Methods for screening for inhibitors of
CC beta secretase activity are also given in the invention. The human
CC aspartase protein and nucleotide sequences and the methods for
CC identifying inhibitors of the protease, are useful in the treatment of
CC and research in to Alzheimer's disease.
XX
SQ Sequence 695 AA;

Query Match 99.7%; Score 3641; DB 21; Length 695;
Best Local Similarity 100.0%; Pred. No. 7.4e-256;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Job time : 40.3333 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:59 ; Search time 18 Seconds
(without alignments)
1638.370 Million cell updates/sec

Title: US-09-806-194-18
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKPPPQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3651	100.0	697	4	US-09-548-372D-18	Sequence 18, Appl
2	3651	100.0	697	4	US-09-548-367D-18	Sequence 18, Appl
3	3651	100.0	697	4	US-09-551-853D-18	Sequence 18, Appl
4	3643	99.8	697	4	US-09-548-372D-16	Sequence 16, Appl
5	3643	99.8	697	4	US-09-548-367D-16	Sequence 16, Appl
6	3643	99.8	697	4	US-09-551-853D-16	Sequence 16, Appl
7	3641	99.7	695	4	US-09-548-372D-12	Sequence 12, Appl
8	3641	99.7	695	4	US-09-548-367D-12	Sequence 12, Appl
9	3641	99.7	695	4	US-09-551-853D-12	Sequence 12, Appl
10	3638	99.6	697	4	US-09-548-372D-20	Sequence 20, Appl
11	3638	99.6	697	4	US-09-548-367D-20	Sequence 20, Appl
12	3638	99.6	697	4	US-09-551-853D-20	Sequence 20, Appl
13	3633	99.5	695	1	US-09-123-702-2	Sequence 2, Appli
14	3633	99.5	695	2	US-08-104-165-1	Sequence 1, Appli
15	3633	99.5	695	3	US-08-464-250-1	Sequence 1, Appli
16	3633	99.5	695	4	US-08-464-250-1	Sequence 1, Appli
17	3633	99.5	695	4	US-09-458-481B-7	Sequence 7, Appli
18	3633	99.5	695	4	US-09-458-481B-8	Sequence 8, Appli
19	3633	99.5	695	4	US-09-548-372D-10	Sequence 10, Appl
20	3633	99.5	695	4	US-09-548-367D-10	Sequence 10, Appl
21	3633	99.5	695	4	US-09-551-853D-10	Sequence 10, Appl
22	3633	99.5	695	6	5218100-2	Patent No. 5218100
23	3628	99.4	695	4	US-09-548-372D-14	Sequence 14, Appl
24	3628	99.4	695	4	US-09-548-367D-14	Sequence 14, Appl
25	3628	99.4	695	4	US-09-551-853D-14	Sequence 14, Appl
26	3627	99.3	694	1	US-08-339-152A-18	Sequence 18, Appl
27	3627	99.3	694	2	US-08-007-999B-5	Sequence 5, Appli
28	3627	99.3	694	2	US-08-689-276A-5	Sequence 5, Appli
29	3621	99.2	695	1	US-08-371-930-27	Sequence 27, Appl
30	3621	99.2	695	5	PCT-US94-01712-27	Sequence 27, Appl
31	3609	98.8	695	1	US-08-339-152A-30	Sequence 30, Appl
32	3604	98.7	753	4	US-09-548-372D-61	Sequence 61, Appl
33	3604	98.7	753	4	US-09-548-367D-61	Sequence 61, Appl
34	3604	98.7	753	4	US-09-551-853D-61	Sequence 61, Appl
35	3594	98.4	751	1	US-08-123-702-4	Sequence 4, Appli
36	3594	98.4	751	2	US-08-104-165-2	Sequence 2, Appli
37	3594	98.4	751	2	US-08-422-333-2	Sequence 2, Appli
38	3594	98.4	751	2	US-08-422-333-21	Sequence 21, Appl
39	3594	98.4	751	3	US-08-464-250-2	Sequence 2, Appli
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41	3594	98.4	751	4	US-08-832-867-5	Sequence 5, Appli
42	3594	98.4	751	4	US-09-548-372D-57	Sequence 57, Appl
43	3594	98.4	751	4	US-09-548-367D-57	Sequence 57, Appl
44	3594	98.4	751	4	US-09-551-853D-57	Sequence 57, Appl
45	3594	98.4	751	6	5187153-2	Patent No. 5187153

ALIGNMENTS

RESULT 1
US-09-548-372D-18
; Sequence 18, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-18

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.1e-265;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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RESULT 2
US-09-548-367D-18
; Sequence 18, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/628CH
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-18

  Query Match           100.0%;  Score 3651;  DB 4;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-265;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
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; Sequence 18, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/628DL
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-18

  Query Match           100.0%;  Score 3651;  DB 4;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-265;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 4
US-09-548-372D-16
; Sequence 16, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapines
US-09-548-372D-16

Query Match 99.8%; Score 3643; DB 4; Length 697;
Best Local Similarity 99.7%; Pred. No. 1.2e-264;

Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 5
US-09-548-367D-16
; Sequence 16, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16

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;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapines
US-09-548-367D-16

  Query Match             99.8%;  Score 3643;  DB 4;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-264;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
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Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 6
US-09-551-853D-16
; Sequence 16, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapines
US-09-551-853D-16

  Query Match             99.8%;  Score 3643;  DB 4;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-264;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 7
US-09-548-372D-12
; Sequence 12, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
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;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-12

  Query Match           99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 8
US-09-548-367D-12
; Sequence 12, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-12

  Query Match           99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 9
US-09-551-853D-12
; Sequence 12, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-12

  Query Match             99.7%;  Score 3641;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 10
US-09-548-372D-20
; Sequence 20, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-20

  Query Match             99.6%;  Score 3638;  DB 4;  Length 697;
  Best Local Similarity   99.6%;  Pred. No. 2.9e-264;
  Matches  694;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 11
US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-20

  Query Match             99.6%;  Score 3638;  DB 4;  Length 697;
  Best Local Similarity   99.6%;  Pred. No. 2.9e-264;
  Matches  694;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 12
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-20

  Query Match             99.6%;  Score 3638;  DB 4;  Length 697;
  Best Local Similarity   99.6%;  Pred. No. 2.9e-264;
  Matches  694;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
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Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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RESULT 13
US-08-123-702-2
; Sequence 2, Application US/08123702
; Patent No. 5604131
; GENERAL INFORMATION:
;   APPLICANT: Wadsworth, Samuel
;   APPLICANT: Snyder, Benjamin
;   APPLICANT: Reddy, Vermuri, B.
;   APPLICANT: Wei, Chamer
;   TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770
; Patent No. 5604131
;   TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Patrea L. Pabst
;   STREET: 2800 One Atlantic Center
;   STREET: 1201 West Peachtree Street
;   CITY: Atlanta
;   STATE: GA
;   COUNTRY: USA
;   ZIP: 30309-3450
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/123,702
;   FILING DATE: 17-SEPT-1993
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Pabst, Patrea L.
;   REGISTRATION NUMBER: 31,284
;   REFERENCE/DOCKET NUMBER: TSI121
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (404)-873-8794
;   TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 695 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-123-702-2

  Query Match   99.5%; Score 3633; DB 1; Length 695;
  Best Local Similarity   99.7%; Pred. No. 6.9e-264;
  Matches 693; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHILKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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RESULT 14
US-08-104-165-1
; Sequence 1, Application US/08104165
; Patent No. 5877015
; GENERAL INFORMATION:
;   APPLICANT: HARDY, John Anthony
;   APPLICANT: GOATE, Alison Mary
;   APPLICANT: MULLAN, Michael John
;   APPLICANT: CHARTIER-HARLIN, Marie-Christine
;   APPLICANT: OWEN, Michael John
;   TITLE OF INVENTION: Test and Model for Alzheimer's Disease
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew

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;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/104,165
;      FILING DATE:  21-JAN-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  9101307.8
;      FILING DATE:  21-JAN-1991
;      APPLICATION NUMBER:  9118445.7
;      FILING DATE:  28-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joe
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  16163-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-104-165-1

  Query Match            99.5%;  Score 3633;  DB 2;  Length 695;
  Best Local Similarity  99.7%;  Pred. No. 6.9e-264;
  Matches  693;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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RESULT 15
US-08-464-250-1
; Sequence 1, Application US/08464250
; Patent No. 6107542
;  GENERAL INFORMATION:
;    APPLICANT:  HARDY, John Anthony
;    APPLICANT:  GOATE, Alison Mary
;    APPLICANT:  MULLAN, Michael John
;    APPLICANT:  CHARTIER-HARLIN, Marie-Christine
;    APPLICANT:  OWEN, Michael John
;    TITLE OF INVENTION:  Test and Model for Alzheimer's Disease
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,250
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/104,165
;      FILING DATE:  21-JAN-1992
;      APPLICATION NUMBER:  9101307.8
;      FILING DATE:  21-JAN-1991
;      APPLICATION NUMBER:  9118445.7
;      FILING DATE:  28-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joe
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  16163-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-250-1

  Query Match            99.5%;  Score 3633;  DB 3;  Length 695;
  Best Local Similarity  99.7%;  Pred. No. 6.9e-264;
  Matches  693;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

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GenCore version 5.1.6

OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-806-194-18
Perfect score: 3651
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	3651	100.0	697	9	US-09-795-847-18	Sequence 18, Appl
3	3651	100.0	697	9	US-09-794-743-18	Sequence 18, Appl
4	3651	100.0	697	9	US-09-794-748-18	Sequence 18, Appl
5	3651	100.0	697	9	US-09-794-925-18	Sequence 18, Appl
6	3651	100.0	697	9	US-09-681-442-18	Sequence 18, Appl
7	3651	100.0	697	11	US-09-869-414-18	Sequence 18, Appl
8	3651	100.0	697	11	US-09-548-366-18	Sequence 18, Appl
9	3643	99.8	697	9	US-09-794-927-16	Sequence 16, Appl
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13	3643	99.8	697	9	US-09-794-925-16	Sequence 16, Appl
14	3643	99.8	697	9	US-09-681-442-16	Sequence 16, Appl
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16	3643	99.8	697	11	US-09-548-366-16	Sequence 16, Appl
17	3641	99.7	695	9	US-09-794-927-12	Sequence 12, Appl
18	3641	99.7	695	9	US-09-795-847-12	Sequence 12, Appl
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21	3641	99.7	695	9	US-09-794-925-12	Sequence 12, Appl
22	3641	99.7	695	9	US-09-681-442-12	Sequence 12, Appl
23	3641	99.7	695	11	US-09-869-414-12	Sequence 12, Appl
24	3641	99.7	695	11	US-09-548-366-12	Sequence 12, Appl
25	3638	99.6	697	9	US-09-794-927-20	Sequence 20, Appl
26	3638	99.6	697	9	US-09-795-847-20	Sequence 20, Appl
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28	3638	99.6	697	9	US-09-794-748-20	Sequence 20, Appl
29	3638	99.6	697	9	US-09-794-925-20	Sequence 20, Appl
30	3638	99.6	697	9	US-09-681-442-20	Sequence 20, Appl
31	3638	99.6	697	11	US-09-869-414-20	Sequence 20, Appl
32	3638	99.6	697	11	US-09-548-366-20	Sequence 20, Appl
33	3633	99.5	695	9	US-09-794-927-10	Sequence 10, Appl
34	3633	99.5	695	9	US-09-795-847-10	Sequence 10, Appl
35	3633	99.5	695	9	US-09-794-743-10	Sequence 10, Appl
36	3633	99.5	695	9	US-09-794-748-10	Sequence 10, Appl
37	3633	99.5	695	9	US-09-794-925-10	Sequence 10, Appl
38	3633	99.5	695	9	US-09-681-442-10	Sequence 10, Appl
39	3633	99.5	695	10	US-09-149-718-2	Sequence 2, Appli
40	3633	99.5	695	11	US-09-869-414-10	Sequence 10, Appl
41	3633	99.5	695	11	US-09-548-366-10	Sequence 10, Appl
42	3633	99.5	695	12	US-09-998-491-1	Sequence 1, Appli
43	3633	99.5	695	12	US-10-357-935-1	Sequence 1, Appli
44	3633	99.5	695	15	US-10-169-580-3	Sequence 3, Appli
45	3628	99.4	695	9	US-09-794-927-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-794-927-18
; Sequence 18, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280PG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 2
US-09-795-847-18
; Sequence 18, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  Patentin Ver. 2.0
; SEQ ID NO 18
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-795-847-18

  Query Match           100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 3.8e-228;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 3
US-09-794-743-18
; Sequence 18, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
```

```
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-748-18

  Query Match             100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-228;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 4
US-09-794-748-18
; Sequence 18, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-748-18

  Query Match             100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-228;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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RESULT 5
US-09-794-925-18
; Sequence 18, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-925-18

  Query Match           100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 3.8e-228;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 6
US-09-681-442-18
; Sequence 18, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-681-442-18

  Query Match           100.0%;  Score 3651;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 3.8e-228;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTITTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTITTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVIPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVIPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 7
US-09-869-414-18
; Sequence 18, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-869-414-18
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  Query Match           100.0%;  Score 3651;  DB 11;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 3.8e-228;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTITTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTITTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 8
US-09-548-366-18
; Sequence 18, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
;  TITLE OF INVENTION:  USES THEREFOR
;  FILE REFERENCE:  28341/6280A
;  CURRENT APPLICATION NUMBER: US/09/548,366
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
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;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 18
;    LENGTH: 697
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-548-366-18

  Query Match           100.0%;  Score 3651;  DB 11;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 3.8e-228;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
US-09-794-927-16
; Sequence 16, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/794,927
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;    LENGTH: 697
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-794-927-16

  Query Match           99.8%;  Score 3643;  DB 9;  Length 697;
  Best Local Similarity  99.7%;  Pred. No. 1.3e-227;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 10
US-09-795-847-16
; Sequence 16, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-795-847-16

  Query Match           99.8%;  Score 3643;  DB 9;  Length 697;
  Best Local Similarity  99.7%;  Pred. No. 1.3e-227;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 11
US-09-794-743-16
; Sequence 16, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-743-16

  Query Match           99.8%;  Score 3643;  DB 9;  Length 697;
  Best Local Similarity  99.7%;  Pred. No. 1.3e-227;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGIK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGIK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 12
US-09-794-748-16
; Sequence 16, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-748-16

  Query Match           99.8%;  Score 3643;  DB 9;  Length 697;
  Best Local Similarity  99.7%;  Pred. No. 1.3e-227;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPIDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPITAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 13
US-09-794-925-16
; Sequence 16, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-925-16

  Query Match             99.8%;  Score 3643;  DB 9;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-227;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 14
US-09-681-442-16
; Sequence 16, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-681-442-16

  Query Match             99.8%;  Score 3643;  DB 9;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-227;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 15
US-09-869-414-16
; Sequence 16, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-869-414-16

  Query Match             99.8%;  Score 3643;  DB 21;  Length 697;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-227;
  Matches  695;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


Search completed: October 2, 2003, 14:18:37
Job time : 41 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:04 ; Search time 16.6667 Seconds
(without alignments)
4021.774 Million cell updates/sec

Title: US-09-806-194-18
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3633	99.5	695	1	A49795	Alzheimer's diseas
2	3582.5	98.1	770	1	QRHUA4	Alzheimer's diseas
3	3536	96.9	695	2	S00550	Alzheimer's diseas
4	3511	96.2	695	2	A27485	Alzheimer's diseas
5	3095	84.8	747	2	JH0773	Alzheimer's diseas
6	2105	57.7	484	4	A32761	hypothetical Alzhe
7	1725	47.2	763	2	A49321	amyloid beta (A4)
8	1709	46.8	765	2	S42880	amyloid precursor-
9	1699	46.5	751	2	A49974	beta-amyloid precu
10	1183	32.4	653	2	A46362	amyloid precursor-
11	1138	31.2	511	2	JC1404	CDEI-box DNA-bindi
12	815.5	22.3	686	2	T15795	hypothetical prote
13	746	20.4	886	2	A32758	beta-amyloid-like
14	706	19.3	246	2	S38344	CDEI-binding prote
15	403	11.0	82	2	PQ0438	Alzheimer's diseas
16	289.5	7.9	191	2	A35981	sperm membrane pro
17	275	7.5	57	2	E60045	Alzheimer's diseas
18	275	7.5	57	2	F60045	Alzheimer's diseas
19	275	7.5	57	2	G60045	Alzheimer's diseas
20	275	7.5	57	2	D60045	Alzheimer's diseas
21	275	7.5	57	2	A60045	Alzheimer's diseas
22	275	7.5	57	2	B60045	Alzheimer's diseas
23	217	5.9	42	2	PN0512	beta-amyloid prote
24	192.5	5.3	1110	2	I51116	NF-180 - sea lampr
25	186	5.1	5170	2	T15348	hypothetical prote
26	185.5	5.1	407	1	EDBEQ3	immediate-early pr
27	185.5	5.1	993	2	S49461	synaptonemal compl
28	182	5.0	522	2	T32444	hypothetical prote
29	175.5	4.8	802	1	S48529	NAB3 protein - yea
30	175.5	4.8	1188	2	T46608	zinc finger protei
31	174	4.8	579	2	JH0820	160K golgi antigen
32	174	4.8	1087	2	T30330	gelsolin-related p
33	172	4.7	675	2	TC3744	myoD protein inhib
34	172	4.7	784	2	PN0009	neurofilament trip
35	172	4.7	1182	2	T30189	myelin transcripti
36	171.5	4.7	793	1	JH0628	caldesmon - human
37	171.5	4.7	884	2	T20405	hypothetical prote
38	171.5	4.7	885	2	G71608	ATP-dept. acyl-CoA
39	171	4.7	1271	2	A45555	glutamate rich pro
40	170	4.7	464	2	H90279	microtubule bindin
41	170	4.7	1948	2	S00485	gene 11-1 protein
42	169.5	4.6	298	1	TPHUTC	troponin T, cardia
43	169.5	4.6	1875	2	S38173	myosin-like protei
44	169	4.6	771	1	A33430	h-caldesmon - chic
45	169	4.6	1187	2	T46637	transcription fact

ALIGNMENTS

RESULT 1
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human suppo
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote
C;Keywords: alternative splicing

Query Match 99.5%; Score 3633; DB 1; Length 695;
Best Local Similarity 99.7%; Pred. No. 1.4e-183;
Matches 693; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTITESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTITESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||| |||||||||||||||||| |||| |||||| ||| ||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 2
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:89392030; PMID:2675637
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral h
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Al
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; And
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; M
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds fo
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-716 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257379
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik,
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovasc
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
```

A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van K
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muell
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PC2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for resic
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for resi
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuth

Query Match 98.1%; Score 3582.5; DB 1; Length 770;
Best Local Similarity 89.9%; Pred. No. 7.2e-181;
Matches 692; Conservative 2; Mismatches 1; Indels 75; Gaps 1;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||||.|||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWIARALEVPIDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||.||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              |||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
```

RESULT 3
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg,
EMBO J. 7, 1365-1370, 1988

```
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brai
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

  Query Match             96.9%;  Score 3536;  DB 2;  Length 695;
  Best Local Similarity   97.0%;  Pred. No. 1.8e-178;
  Matches  674;  Conservative    8;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
Db        541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db        601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 4
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzhe
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C;Keywords: alternative splicing; amyloid; transmembrane protein

  Query Match             96.2%;  Score 3511;  DB 2;  Length 695;
  Best Local Similarity   96.5%;  Pred. No. 3.6e-177;
  Matches  671;  Conservative    6;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWGVADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLDLENYIIALQAVPPRPHHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKATQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSTHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
```

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match   84.8%; Score 3095; DB 2; Length 747;
  Best Local Similarity   80.8%; Pred. No. 2.9e-155;
  Matches 596; Conservative   36; Mismatches   42; Indels   54; Gaps   5;

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Qy         17 ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQE 75
              |||  ||| |||||||||||   |||||||||||||:|| ||  || |||:|||||  |
Db         15 ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE 71

Qy         76 VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF 135
              ||||||||||||||||||||:|||||:  | :|||||||||||||||||||||||||||
Db         72 VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF 131

Qy        136 LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN 195
              |||||||:|||||||||||||:|||| :||:|||||||||||||||||'| |.|::
Db        132 LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEESES 191

Qy        196 VDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDEDDEDGDE 253
               ||||| ||| |||||||| || | |:|| ||    |'|:|| |||||| || ||  |'||
Db        192 FDSADAAEDDCDVWWGGADADYVDRSDDKAVEAQPDEEEEVVEVEEEEETDDDED--DGDE 249

Qy        254 VEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------------------------- 288
              ||| ||||||||||:|||||||||||:||||||||
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Db        250 AEEEPEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYYDVTE 309

Qy        289 ------------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQ 317
                                           :| |||||||||||||| | |||||  |
Db        310 SKCAQFIYGGCGGNRNNFESDDYCMAVCGSVIPATAASTPDAVDKYLENPNDENEHDRFL 369

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQ 377
              ||||||| ||||:||:|:|:|||||||||||||||||||||||||||||||||||| :|||
Db        370 KAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ 429

Qy        378 LVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 437
              |||||||||||||||||:|||||||||||| |||||||||||||||||||||||||||||
Db        430 LVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 489

Qy        438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNY 497
              :|||||||||||||||||:|||| |||||| |||| |||||||:|||||: |||:||
Db        490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAVAEEIQDEVDELFQKEQNY 549

Qy        498 SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAN 557
              |||:::|||:: |:|:||||||||||:|||||||||:||  :::|||'|||||| ||||||
Db        550 SDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPWHSFGVDSVPAN 609

Qy        558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFA 617
              |||||||||||||||||||||||||||||||||||||||||||| :|:|:|||: ||||||||||
Db        610 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669

Qy        618 EDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKM 677
              |:|||||||||||||||||||||||||||||||||||:|||||:|||||||||||||||:||
Db        670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHHGVVEVDAAVTPEERHLTKM 729

Qy        678 QQNGYENPTYKFFEQMQN 695
              ||||| ||||| ||||||
Db        730 QQNGYENPTYKFFEQMQN 747
```

RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - hum
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C;Accession: A32761
R;de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A;Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secr
A;Reference number: A32761; MUID:89346754; PMID:2569763
A;Accession: A32761
A;Molecule type: mRNA
A;Residues: 1-484 <DES>
A;Cross-references: GB:M28373
A;Note: the authors translated the codon ATG for residue 433 as Leu
C;Comment: This is the hypothetical translation of a sequence believed to contain
C;Keywords: cloning artifact

  Query Match   57.7%; Score 2105; DB 4; Length 484;
  Best Local Similarity   87.7%; Pred. No. 1.7e-103;
  Matches 407; Conservative   1; Mismatches   0; Indels   56; Gaps   1;

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Qy         80 LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQE 139
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQE 60

Qy        140 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 199
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 120

Qy        200 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAE 259
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAE 180

Qy        260 EPYEEATERTTSIATTTTTTTESVEEVVR---------------------------- 288
              ||||||||||||||||||||||||||||
Db        181 EPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPF 240
```

```
Qy        289 ----------------     -----VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 323
                                   :||||.|||||| |||:|||||. ||||||.|||
Db        241 FYGGCGGNRNNFDTEEYCMAVCGSAIPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 300

Qy        324 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM 383
              |||||||||||||||||.|||||||||:|||| ||| |.|||:.||||| ||||: ||| |
Db        301 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM 360

Qy        384 ARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 443
              |||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||.|||
Db        361 ARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 420

Qy        444 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV 487
              ||||||||||||||||||||||||||||||||||||||||||||
Db        421 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV 464


RESULT 7
A49321
amyloid beta (A4) homolog 2 precursor - human
N;Alternate names: CDEI-binding protein
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49321; S34644; S40519
R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
A;Reference number: A49321; MUID:93250009; PMID:8485127
A;Accession: A49321
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <SPR>
A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)
A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A;Description: The human homologue of the murine CDEI binding protein is an amyloid prec
A;Reference number: S34644
A;Accession: S34644
A;Molecule type: mRNA
A;Residues: 1-763 <VON>
A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A;Reference number: S40519; MUID:94035131; PMID:8220435
A;Accession: S40519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <WAS>
A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C;Genetics:
A;Gene: GDB:APLP2; APPL2
A;Cross-references: GDB:139159; OMIM:104776
A;Map position: 11q23-11q25
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; transmembrane protein
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             47.2%;  Score 1725;  DB 2;  Length 763;
  Best Local Similarity   46.9%;  Pred. No. 2.9e-83;
  Matches  369;  Conservative  112;  Mismatches  170;  Indels  136;  Gaps   19;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | ||||   || || :         |||    :|.|||||||:||||:|:: |||: ||
Db         15 LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:| :||| :|||:|||:|||||||||:|||| |:' |||:| :|||:   |: |::
Db         75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||||||||| ||:|:||:| ::|||:||| | ||||| || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|||| :   :|  : |||:          : :  |  ||  |  :|    /:
Db        193 DQFHGIEYVCCPQTKIIGSVSKEEEEEDEE-------EEEEEDEFEDYDVYKSEFPTEAD 245

Qy        237 VEE--EEA--DDDEDDEDGDEVEEEAEEPY----------EEATERTTSIATTTTTTTES 282
              :|:  | |  :|||||:|:|:|| |: :  |           |  ||  :    :    |
Db        246 LEDFTEAAVDEDDEDEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy        283 VEEV-------------------------------------------------VRVP 290
              |: |                                                  :|
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMIP 365

Qy        291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAEKQAKNLPK 350
              |  | | || | ||  |:|||| |||||||:|| :|| || :| :|||'|| |||||||
Db        366 PTPLPTND-VDVYFEISADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy        351 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPP 410
              |::: :|||||  |:|||:|||:|:|||||||:|||||||||||||:|||:|:: ||| ||
Db        425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP 484

Qy        411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 470
              ||  :   |:::|||| ||| ||:::|::|  |||:|||::|||||| || || ||||
Db        485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSL 544

Qy        471 SLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVE 530
              |||| || ||:|||:|:|||||:::       |:|          |    |:::||  |
Db        545 SLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTASISETPVDVR 587

Qy        531 LLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPG-----SGLIN 585
                .: | | ::: |:| |     ||  |||    | :|     :   |        ||
Db        588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPMKKGSGVGEQDGGLIG 637

Qy        586 IKTEEISEVN-LDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKGAI 627
              : : |:  | :|     |   :|  ::::| || ||                  :  |:
Db        638 AEEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEEERESVGPLREDFSLSSSAL 695

Qy        628 IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTY 687
              ||::|  | |||||||:||||:|:|| :| ||:|||  :|||||||:||| :|||||||
Db        696 IGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENPTY 755

Qy        688 KFFEQMQ 694
              |: ||||
Db        756 KYLEQMQ 762


RESULT 8
S42880
amyloid precursor-like protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S42880; S47528
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A;Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid p
A;Reference number: S42880
A;Accession: S42880
A;Molecule type: mRNA
A;Residues: 1-765 <SAN>
A;Cross-references: EMBL:X77934
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protei
A;Reference number: S47528; MUID:94368849; PMID:8086458
A;Accession: S47528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-765 <SA2>
A;Cross-references: EMBL:X77934
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
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```
C;Keywords: alternative splicing
F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match          46.8%;  Score 1709;  DB 2;  Length 765;
  Best Local Similarity   45.9%;  Pred. No. 2e-82;
  Matches  361;  Conservative  124;  Mismatches  168;  Indels  134;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGIKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
Db        133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYA-DGSEDKVVEVAEEEE 235
Db        193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEE----DEEEDYALDKSEFPTEADLEDFT 248

Qy        234 VAEVEEEEADDDEDDEDGDEVEEEAEEPYEE------ATERTTSIATTTTTTTESVEEVV 287
Db        249 EAAADEDEDEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV 308

Qy        288 R-----------------------------------------------------VPT 291
Db        309 KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMIPP 366

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
Db        369 TPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRSRMDRVKKEWEEAELQAKNLPKA 427

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
Db        428 ERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYLAALQSDPPR 487

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
Db        488 PHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSLS 547

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
Db        548 LLYKVPYVAQEIQEEIDELLQEQR-------ADM---------DQFTSSISENPVDVR- 589

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARP------AADRGLTTRPGSGLTN 585
Db        590 --VSSEES-EEIPPFHPF--HPFPSLSENE----DTQPELYHPMKKGSGMAEQDG-GLIG 639

Qy        586 IKTEEISEVN-LDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKGAI 627
Db        640 AEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPDSVGPLREDFSLSSSAL 697

Qy        628 IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTY 687
Db        698 IGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPMLTPEERHLNKMQNHGYENPTY 757

Qy        688 KFFEQMQ 694
Db        758 KYLEQMQ 764
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RESULT 9
A49974
beta-amyloid precursor protein 2 homolog APLP2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49974
R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
A;Reference number: A49974; MUID:94132029; PMID:8300594
A;Accession: A49974
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-751 <SLU>
A;Cross-references: GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558468
A;Note: sequence extracted from NCBI backbone (NCBIP:144636)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

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  Query Match          46.5%;  Score 1699;  DB 2;  Length 751;
  Best Local Similarity   45.6%;  Pred. No. 6.4e-82;
  Matches  361;  Conservative  114;  Mismatches  160;  Indels  156;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE---E 231
Db        193 DQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEFPTE 243

Qy        232 EEVAEVEEEEAD-DDEDDEDGDEVEEE------- ------AEEPYEEATERTTSIATTT 276
Db        244 ADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNEENPTEPSSEGTIS----- 298

Qy        277 TTTTESVEEV----------------------------------------------- 286
Db        299 --DKEIVHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYC 356

Qy        287 -----VRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
Db        357 MAVCKAMIPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEA 415

Qy        342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENY 401
Db        416 ELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENY 475

Qy        402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
Db        476 LAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHV 535

Qy        462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 521
Db        536 IEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-------ADM---------DQFTSS 578

Qy        522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGS 581
Db        579 ISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQDG- 621

Qy        582 GLTNIKTEEISEVN-LDAEFRHDSGYEVHHQKLVFFAEDVGS----------------N 623
Db        622 GLIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFSLS 679

Qy        624 KGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYE 683
Db        680 SNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYE 739

Qy        684 NPTYKFFEQMQ 694
Db        740 NPTYKYLEQMQ 750
```

RESULT 10
A46362

```
amyloid precursor-like protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A46362
R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
A;Title: Identification of a mouse brain cDNA that encodes a protein related to the Alz
A;Reference number: A46362; MUID:93066322; PMID:1279693
A;Accession: A46362
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-653 <WAS>
A;Experimental source: brain
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: transmembrane protein

  Query Match             32.4%;  Score 1183;  DB 2;  Length 653;
  Best Local Similarity   39.0%;  Pred. No. 6.9e-55;
  Matches  275;  Conservative  121;  Mismatches  221;  Indels   88;  Gaps   20;

Qy          1 MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGT 59
              :|| |:|||| | |  | | :  |     |:  |||' :| ::: |:': |'  :
Db         22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy         60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
              : |:   : :|:|||:::|||| |  | :| | : :: ||   |     ||| |:.: ||
Db         81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAIPMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy        119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
              |||||:|||||: |:|||||||| ||:    | |:| '| :   || |||||||, |:
Db        141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDR 200

Qy        179 FRGVEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
              |||||:||||    : |     | :  :  | ||     |:| ||       ||||
Db        201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-------EEEVESF 248

Qy        238 EEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATITTTTTIESVEEVVRVPTTAASTP 297
              :  |   :    :| ||| ||     :  |  : :  | |          ||
Db        249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR--------PI------- 294

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              | || :   ||:  ||  | :||  || :   :::::|'||   ': |:| |||:::::|:
Db        295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              : |:  :::|::: : |:|:||:|  |  |:::|:: | |||  :: ,|' | :  |
Db        355 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |::|:|||||:::::|:|:::|.  ||||:.| |:| || |||:|| : |||'| ||   :
Db        415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMP-SLIETKTTVELLPVNG 536
              :|:|:: :: |||          || :    :    || :| | :' |
Db        475 HLAQELRPQIQELL----------LAEHLGPSEL----DASVPGSSSFDK---------- 510

Qy        537 EFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADPGLIIRPGSG-----LTNIKTEET 591
                  |||             |:: :    |   :| | :  |      :' ::
Db        511 ----GSLQP-----------PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYE- 550

Qy        592 SEVNLDAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML 648
              :||  |      |:  |   |:        | :: |: |||:  |    ::||::|:|
Db        551 QKVNASA----PRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSMVLSLLL 606

Qy        649 -KKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPIYKFFEQ 692
              |:| | :| ||||||:  :| ||: | ::|::;||||||:| ':
Db        607 RKKKPYGTISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 651


RESULT 11
JC1404
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```
CDEI-box DNA-binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C;Accession: JC1404
R;Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
A;Title: A murine sequence-specific DNA binding protein shows extensive local simi
A;Reference number: JC1404; MUID:93129193; PMID:1482349
A;Accession: JC1404
A;Molecule type: mRNA
A;Residues: 1-511 <VID>
C;Comment: This protein plays an important role in the early development of the mo
C;Keywords: DNA binding; transmembrane protein

  Query Match             31.2%;  Score 1138;  DB 2;  Length 511;
  Best Local Similarity   45.4%;  Pred. No. 1.2e-52;
  Matches  251;  Conservative   93;  Mismatches  129;  Indels   80;  Gaps   16;

Qy        174 CGIDKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE- 230
              ||:|:| | |:|||  :  :|||:  | : |||:           | |  ||  :: :|
Db          6 CGVDQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEF 56

Qy        231 --EEEVAEVEEEEAD-DDEDDEDGDEVEEEAE--------EPYEEATERTTSIATTTTTT 279
                | :: :  |  || ::||:|:|:|| |: :        : | |  |  |  ::  | :
Db         57 PTEADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTIS 114

Qy        280 TESVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWE 339
                :  :   |:|| |   | | |: | ||  |:|||| ||||||:|| :|| || :| ::||
Db        115 DKEIVHDVKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWE 173

Qy        340 EAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALE 399
              ||| |||||:|| ::: :|||||  |::||:|||:|:|||||||:|||||||||:|||
Db        174 EAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALE 233

Qy        400 NYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHL 459
              ||: |||: |||| :   |::|||| ||| ||:|:|:|  |||:|||::|||||,
Db        234 NYLAALQSDPPRPRHILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHL 293

Qy        460 RVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALM 519
              || || |:|||||| || ||:|||:|:|||||::       |:|          |
Db        294 HVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFT 336

Qy        520 PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRP 579
              |::|  | :    |  :   | | |     |: :|||           |:  :
Db        337 SSISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQD 380

Qy        580 GSGLTNIKTEEISEVN-LDAEFRHDSGYEVHHQKLVFFAEDVGS---------------- 622
              | ||   : : |:  | :|     |   :|  ::::| |: ||
Db        381 G-GLIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFS 437

Qy        623 -NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNG 681
               :  |:|||:|  | |||||||:||||:|:|| :| |::|||  :|||||:|:||| :|
Db        438 LSSNALIGLLVIAVAIAIVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHG 497

Qy        682 YENPTYKFFEQMQ 694
              |||||||: ||||
Db        498 YENPTYKYLEQMQ 510


RESULT 12
T15795
hypothetical protein C42D8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C;Accession: T15795; A49414
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C42D8.
A;Reference number: Z18405
A;Accession: T15795
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-686 <HAL>
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```
A;Cross-references: EMBL:U56966; NID:g1293844; PID:g1293850; PIDN:AAA98722.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone C42D8
R;Daigle, I.; Li, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993
A;Title: apl-1, a Caenorhabditis elegans gene encoding a protein related to the human be
A;Reference number: A49414; MUID:94089766; PMID:8265668
A;Accession: A49414
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-686 <DAI>
A;Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297
C;Genetics:
A;Gene: CESP:C42D8.8
A;Map position: X
A;Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 580/3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

  Query Match             22.3%;  Score 815.5;  DB 2;  Length 686;
  Best Local Similarity   29.1%;  Pred. No. 1.5e-35;
  Matches  222;  Conservative  109;  Mismatches  276;  Indels  155;  Gaps   22;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKEIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63

Qy         61 ICIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKIHPHFVIPYRCLVG 120
Db         64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN-----LHDYGMLLPC 174
Db        123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy        175 GIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV 234
Db        183 ALDMFTGVEFVCCP----NDQTNKTDVQKTK---------------------------- 209

Qy        235 AEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTIAA 294
Db        210 ---EDEDDDDEDDAYEDDYSEESDEKDEE------------------------------ 236

Qy        295 STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA-----ERQAKNLP 349
Db        237 -EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHRKKVDKVMKEWGDLETRYNEQKAKD-P 294

Qy        350 KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL- 405
Db        295 KGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA 354

Qy        406 -QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE 464
Db        355 THVNKPNKHSVLQSLKAYIRAEEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL 414

Qy        465 RMNQSLSLLYNVP---------AVA--EEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
Db        415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE----DSELTPIIHDDEFSK 470

Qy        514 GN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANT---ENEVEP 564
Db        471 NAKLDVKAPTTTAKPVKETDNAKVLPTEASDSEEEADEYYEDEDDEQVKKTPDMKKKVKV 530

Qy        565 VDARP--------------------AADRGLTTRPGSGLTNIKTEE-----ISEVNLDA 598
Db        531 VDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSSESDEDEDKNIKELRVDI 590

Qy        599 E---------FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 649
Db        591 EPIIDEPASFYRHD--------KLIQSPEVERSASSVFQPYVLASAMFITAICIIAFAIT 642

Qy        650 KKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
Db        643 NARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFFD 683
```

```
RESULT 13
A32758
beta-amyloid-like protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 24-Sep-1998
C;Accession: A32758
R;Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989
A;Title: A Drosophila gene encoding a protein resembling the human beta-amyloid pr
A;Reference number: A32758; MUID:89184650; PMID:2494667
A;Accession: A32758
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-886 <ROS>
A;Cross-references: GB:J04516; NID:g158371; PID:g158372
C;Genetics:
A;Gene: FlyBase:Appl
A;Cross-references: FlyBase:FBgn0000108
C;Keywords: transmembrane protein

  Query Match             20.4%;  Score 746;  DB 2;  Length 886;
  Best Local Similarity   25.5%;  Pred. No. 9.3e-32;
  Matches  233;  Conservative  126;  Mismatches  289;  Indels  264;  Gaps   29;

Qy          7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDSDPSG 58
Db          9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVTDLSK 63

Qy         59 T---KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
Db         64 KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWI 123

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
Db        124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRTFAMLL 182

Qy        173 PCGIDKFRGVEFVCCP---------------------------LAEESDNVD---SA 199
Db        183 PCGISVFSGVEFVCCPKHFKTDEIHVKKTDLPVMPAAQINSANDELMNDEDDSNDSNYSK 242

Qy        200 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV--------------------AEV 237
Db        243 DANEDDLD------DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINAEY 296

Qy        238 EE-EEADDDEDDEDGDEVEEEAEEPY-------------------------EEATERT 269
Db        297 DSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLKSDSSSPSSAPVAPAPEKAPVKS 356

Qy        270 TSIATTTTTTESVEEVV-----------RVPTTAASTPDAVDKYLETPGDENEHAHFQK 318
Db        357 ESVTSTPQLSASAAAFVAANSGNSGTGAGAPPSTAQPTS---DPYFTHFDPHYEHQSYKV 413

Qy        319 AKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKA-------VIQHFQEKVESLEQEA 371
Db        414 SQKRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFKQRMTARFQTSVQALEEEG 473

Qy        372 ANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQ 431
Db        474 NAEKHQLAAMHQQRVLAHINQRKREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDRA 533

Qy        432 HTLKHFEH-VRMVDP---KKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI---- 483
Db        534 HALAHYRHLLNSGGPGGLEAAASERPRTLERLIDIDRAVNQSMTMLKRYPELSAKIAQLM 593

Qy        484 ---------QDEV-------------------------------------------- 487
Db        594 NDYILALRSKDDIPGSSLGMSEEAEAGILDKYRVEIERKVAEKERLRLAEKQRKEQRAAE 653

Qy        488 -----DELLQKEQNYSDDVLANMISE---------------------PRISYGNDALM 519
Db        654 REKLREEKLRLEAKKVDDMLKSQVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAAL 713
```

```
Qy        520 -----PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRG 574
                   |:|  ||:           | | | :    :|  :        |         :  |
Db        714 VTAANPNLETTKS---------EKDLSDTE----YGEATVSTTKVQTVLPTVDDDAVQRA 760

Qy        575 LTTRPGSGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---GA 626
                 :    :       ::     : : :|   ::: |::  |       ||:     :
Db        761 VEDVAAA---------VAHQEAEPQVQHFMTHDLGHRESSFSLRREFAQHAHAAKEGRNV 811

Qy        627 IIGLMVGGVVIATVIVITLVMLKKKQYTSIH-HGVVEVDAAVTP------EERHLSKMQQ 679
                  |    |: :   : : : : | :    |  |  | :||.  ||        .|: :  ||
Db        812 YFTLSFAGIALMAAVFVGVAVAKWRTSRSPHAQGFIEVDQNVTTHHPIVREEKIVPNMQI 871

Qy        680 NGYENPTYKFFE 691
              ||||!|||||:||
Db        872 NGYENPTYKYFE 883
```

RESULT 14
S38344
CDEI-binding protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1996
C;Accession: S38344
R;Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.
Biochim. Biophys. Acta 1216, 154-156, 1993
A;Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
A;Reference number: S38344; MUID:94032480; PMID:8218408
A;Accession: S38344
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-246 <HAN>
A;Cross-references: EMBL:Z22592
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

```
  Query Match             19.3%;  Score 706;  DB 2;  Length 246;
  Best Local Similarity   51.5%;  Pred. No. 2.4e-30;
  Matches  136;  Conservative   35;  Mismatches   51;  Indels   42;  Gaps    7;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
               | :|||   || |  :         |||     :'|||||, ||:|:||:::| |||: ||
Db         15 LLVLLLLGLTAPAALAGYIEALAANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: |||  :||||||:|||||||||:||||||||   :|||: ::|||:  | |||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||:||| |||||  |::  ||||:|||  .  |||: :| |    :: |||:'|||:
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|:|     ::  |||                          |   :      · |
Db        193 DQFHGTEYVCCP---QTKTVDS------------------------DSTMSKEEEE--- 222

Qy        237 VEEEEADDDED-DEDGDEVEEEAE 259
               ||:| |::|| | |  |   ||:
Db        223 -EEDEEDEEEDYDLDKSEFPTHAD 245
```

RESULT 15
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide i
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

```
  Query Match             11.0%;  Score 403;  DB 2;  Length 82;
  Best Local Similarity   97.6%;  Pred. No. 5e-15;
  Matches   80;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        581 SGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATV 640
              |:|||||||||||| :|||||:||||||||||||||||||||||||:|||||:|||'||||||
Db          1 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATV 60

Qy        641 IVITLVMLKKKQYTSIHHGVVE 662
              |||:|||||||||||||||||::
Db         61 IVITLVMLKKKQYTSIHHGVVE 82
```

Search completed: October 2, 2003, 14:00:33
Job time : 18.6667 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:24 ; Search time 10 Seconds
(without alignments)
3277.761 Million cell updates/sec

Title: US-09-806-194-18
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3582.5	98.1	770	1	A4_HUMAN	P05067 h amyloid b
2	3582.5	98.1	770	1	A4_MACFA	P53601 m amyloid b
3	3576	97.9	751	1	A4_SAISC	Q95241 s amyloid b
4	3527.5	96.6	770	1	A4_PIG	P79307 s amyloid b
5	3514.5	96.3	770	1	A4_CAVPO	Q60495 c amyloid b
6	3485.5	95.5	770	1	A4_MOUSE	P12023 m amyloid b
7	3485.5	95.5	770	1	A4_RAT	P08592 r amyloid b
8	1730	47.4	695	1	APP2_MOUSE	Q06335 mus musculu
9	1725	47.2	763	1	APP2_HUMAN	Q06481 homo sapien
10	1709	46.8	765	1	APP2_RAT	P15943 rattus norv
11	1191	32.6	650	1	APP1_HUMAN	P51693 homo sapien
12	1183	32.4	653	1	APP1_MOUSE	Q03157 mus musculu
13	815.5	22.3	686	1	A4_CAEEL	Q10651 caenorhabdi
14	747.5	20.5	887	1	A4_DROME	P14599 drosophila
15	284	7.8	59	1	A4_BOVIN	Q28053 bos taurus
16	280	7.7	58	1	A4_RABIT	Q28748 oryctolagus
17	280	7.7	58	1	A4_SHEEP	Q28757 ovis aries
18	279	7.6	58	1	A4_CANFA	Q28280 canis famil
19	275	7.5	57	1	A4_URSMA	Q29149 ursus marit
20	185.5	5.1	407	1	IE68_HSVSA	Q01042 herpesvirus
21	185.5	5.1	993	1	SCP1_MOUSE	Q62209 mus musculu
22	176	4.8	2004	1	MOZ_HUMAN	Q92794 homo sapien
23	175.5	4.8	802	1	NAB3_YEAST	P38996 saccharomyc
24	174	4.8	579	1	G160_HUMAN	Q08378 homo sapien
25	171.5	4.7	793	1	CALD_HUMAN	Q05682 homo sapien
26	169.5	4.6	297	1	TRT2_HUMAN	P45379 homo sapien
27	169.5	4.6	1875	1	MLP1_YEAST	Q02455 saccharomyc
28	169	4.6	771	1	CALD_CHICK	P12957 gallus gall
29	168	4.6	721	1	YCF2_OENPI	P31568 oenothera p
30	167.5	4.6	816	1	YG3A_YEAST	P53278 saccharomyc
31	167	4.6	1240	1	YNJ1_YEAST	P53935 saccharomyc
32	166.5	4.6	681	1	MP10_HUMAN	O00566 homo sapien
33	164	4.5	2017	1	MYSN_DROME	Q99323 drosophila
34	163.5	4.5	1976	1	MYHA_HUMAN	P35580 homo sapien
35	162.5	4.5	712	1	NUCL_RAT	P13383 rattus norv
36	162.5	4.5	1325	1	G160_MOUSE	P55937 mus musculu
37	162.5	4.5	1332	1	SPT7_YEAST	P35177 saccharomyc
38	161.5	4.4	1976	1	MYHA_RAT	Q9jlt0 rattus norv
39	160.5	4.4	1955	1	PUMA_PARUN	O61308 parascaris
40	158	4.3	301	1	TRT2_CHICK	P02642 gallus gall
41	157.5	4.3	1976	1	MYHA_BOVIN	Q27991 bos taurus
42	157	4.3	706	1	NUCL_HUMAN	P19338 homo sapien
43	156.5	4.3	5596	1	MDN1_HUMAN	Q9nu22 homo sapien
44	156	4.3	694	1	NUCL_CHICK	P15771 gallus gall
45	155.5	4.3	747	1	KF3B_HUMAN	O15066 homo sapien

ALIGNMENTS

RESULT 1
A4_HUMAN
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q9BT38;
AC Q9UCB6; Q9UQ58;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracelluiar domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";

RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [10]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [11]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [12]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).

RN [13]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [15]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [16]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [17]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [18]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [19]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [20]
RP SEQUENCE OF 672-681.
RC TISSUE=Brain cortex;
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [21]
RP SEQUENCE OF 674-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease.";

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  Query Match             98.1%;  Score 3582.5;  DB 1;  Length 770;
  Best Local Similarity   89.9%;  Pred. No. 4.1e-171;
  Matches  692;  Conservative    2;  Mismatches    1;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||:||||||||||||.||||||||||||||||.|||||:|||||'|||'||||||·|||:
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||:||||||||||·||||||||:|||||||·||||||||||| |||:|||||' |||.
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||:||||||.|||||.||||:|||||||||:||||| |||'|||||| |||:
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||:||||||||||||:|:||||||:|||||:||||.||| |||||:.!||:'|||:||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||:||||||||||||| |||||||||||||||||||| |||:|'||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 -------------------------------------------------------------- 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||'|||||||||||||.:||||:||||||||.|||·:'|||: |||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||:|||||'|||||||||||||||||.||||:|||||·: |||·||||  ||||:.||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||:||||||||||||||||||||||||||||||:|||||'||||· |||||·||| |||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              |:||||||:|||||||:||||||||||||:|||||||:|||||'.|||||||||'||||:
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||:|||||||||||||||||||||||||:||||||||||||||:|||||:'|||||.|||·|:
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              ||||||||: :|||||||||||||||||||||||||||||·||||||||||||||:||||:||||:
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 2
A4_MACFA

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ID   A4_MACFA       STANDARD;      PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
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CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL       1     17       BY SIMILARITY.
FT   CHAIN       18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN       18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN       18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN      672    770       C99 (POTENTIAL).
FT   CHAIN      672    713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN      672    711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN      688    770       C83 (POTENTIAL).
FT   CHAIN      688    713       P3(42) (POTENTIAL).
FT   CHAIN      688    711       P3(40) (POTENTIAL).
FT   CHAIN      712    770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN      714    770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN      721    770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN      740    770       C31 (POTENTIAL).
FT   DOMAIN      18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   700    723       POTENTIAL.
FT   DOMAIN     724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN     291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN     391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN     732    751       INTERACTION WITH G(O)-ALPHA
FT                               (BY SIMILARITY).
FT   DOMAIN     230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN     274    280       POLY-THR.
FT   SITE       144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                               (BY SIMILARITY).
FT   ACT_SITE   301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE       671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE       672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE       687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE       704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                               (BY SIMILARITY).
FT   SITE       706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                               (BY SIMILARITY).
FT   SITE       711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                               (BY SIMILARITY).
FT   SITE       713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                               (BY SIMILARITY).
FT   SITE       720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                               (BY SIMILARITY).
FT   SITE       724    734       BASOLATERAL SORTING SIGNAL
FT                               (BY SIMILARITY).
FT   SITE       739    740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                               (BY SIMILARITY).
FT   SITE       757    760       ENDOCYTOSIS SIGNAL.
FT   SITE       759    762       NPXY MOTIF.

  Query Match             98.1%;  Score 3582.5;  DB 1:  Length 770;
  Best Local Similarity   89.9%;  Pred. No. 4.1e-171;
  Matches  692;  Conservative    2;  Mismatches    1;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTITTTTTESVEEVVR------------ 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLRKTTREPLTRD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
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Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||.|||||.|||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              |||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||.|.|||||'||||||||||'|.||||| ||||| |||||'|||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 3
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      316    344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      363    428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      504    521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      713    732       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND.
FT   SITE        652    653       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        653    654       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        668    669       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        685    685       INVOLVED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        687    687       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        692    693       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        694    695       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        701    702       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                (BY SIMILARITY).
FT   SITE        705    715       BASOLATERAL SORTING SIGNAL
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                (BY SIMILARITY).
FT   SITE        738    741       ENDOCYTOSIS SIGNAL.
FT   SITE        740    743       NPXY MOTIF.
FT   METAL       137    137       COPPER (BY SIMILARITY).

  Query Match             97.9%;  Score 3576;  DB 1;  Length 751;
  Best Local Similarity   91.7%;  Pred. No. 8.5e-171;
  Matches  689;  Conservative    3;  Mismatches    3;  Indels   56;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDHVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIAITTTTTTTESVEEVVR------------ 288
              ||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ----------------------------------------------VPTTAASTPDAVDKYL 304
                                                           :|||||:|||||||||
Db        301 RAMISRWYFDVIEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVIPTTAASTPDAVDKYL 360

Qy        305 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 420

Qy        365 ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR 424
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db        421 ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR 480

Qy        425 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ 484
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        481 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ 540

Qy        485 DEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 600

Qy        545 PWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKLDAEFRHDS 604
              |||||||||||||||||||||||||||||||||||||||||||||||||| :||||||||
Db        601 PWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 660

Qy        605 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 720

Qy        665 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||
Db        721 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751


RESULT 4
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
```

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DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dabl (By similarity). Binding
CC       to Dabl inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
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DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       C83 (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59).
FT   CHAIN       714    770       GAMMA-CTF(57).
FT   CHAIN       721    770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135    155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA (BY
FT                                SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).

  Query Match             96.6%;  Score 3527.5;  DB 1;  Length 770;
  Best Local Similarity   88.2%;  Pred. No. 2.2e-168;
  Matches  679;  Conservative    9;  Mismatches    7;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||:||:||||||||||||||||||||||||||:|||||:|||||||||||||:|||||
Db          1 MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| ||||||||||||||||||||||||||||||||||||:|||||| | :|||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||:|:|||||||||||||||||||||||||||||||||||||| |||||
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||:|||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLLKTTQEHLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||||| || ||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              |||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770


RESULT 5
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
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RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, PPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via HaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clatherin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC       sulfate to the L-APP isoforms produces the APP proteoglycan core
CC       proteins, the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (BY SIMILARITY).

  Query Match             96.3%;  Score 3514.5;  DB 1;  Length 770;
  Best Local Similarity   87.9%;  Pred. No. 9.9e-166;
  Matches  677;  Conservative    8;  Mismatches   10;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||| ;|||||||||||||||||||||||||||||||||| ||||| ||| |||||
Db          1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWEPDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| :|||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||:|||||||||| |||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              ||||||| |||||||||||||.||||:|||||||||||||||||||||
Db        241 EADDDEDVEDGDEVEEEAEEPYEEATEKTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RSMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQNLLKTSGEPVSQG 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              |||||:|,|||||'||||||'||||||||||||||||||,|||||:|||| '|||||,|||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              |||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              |||||||| :|||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 6
A4_MOUSE
ID   A4_MOUSE        STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN [8]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [9]
RP SEQUENCE OF 656-737 FROM N.A.
RC STRAIN=129/Sv;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA Loring J.F., Goate A.M.;
RT "Introduction of six mutations into the mouse genome using 'Hit and
RT Run' gene-targeting: introduction of familial Alzheimer's disease
RT mutations into the mouse amyloid precursor protein gene and
RT humanization of the A-beta fragment.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX PubMed=8510506;
RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT "Regional distribution of the alternatively spliced isoforms of beta
RT APP RNA transcript in the brain of normal, heterozygous and
RT homozygous weaver mutant mice as revealed by in situ hybridization
RT histochemistry.";
RL Brain Res. Mol. Brain Res. 17:340-346(1993).
RN [11]
RP INTERACTION WITH KNS2.
RX PubMed=11144355;
RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT "Axonal transport of amyloid precursor protein is mediated by direct
RT binding to the kinesin light chain subunit of kinesin-I.";
RL Neuron 28:449-459(2000).
RN [12]
RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP THR-743; TYR-757; ASN-759 AND TYR-762.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [13]
RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX MEDLINE=22028091; PubMed=11912189;
RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT with scaffold proteins of the JNK signaling cascade.";
RL J. Biol. Chem. 277:20070-20078(2002).
RN [14]
RP INTERACTION OF CTF PEPTIDES WITH NUMB.
RX PubMed=12011466;
RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT "The gamma-secretase-generated intracellular domain of beta-amyloid
RT precursor protein binds Numb and inhibits Notch signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN [15]
RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX PubMed=11553691;
RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT gamma-secretase is rapidly degraded but distributes partially in a
RT nuclear fraction of neurones in culture.";
RL J. Neurochem. 78:1168-1178(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions. Can promote transcription activation through binding
CC to APBB1/Tip60 and inhibit Notch signaling through interaction
CC with Numb. Couples to apoptosis-inducing pathways such as those
CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
CC similarity). Acts as a kinesin I membrane receptor, mediating the
CC axonal transport of beta-secretase and presenilin 1. May be
CC involved in copper homeostasis/oxidative stress through copper ion
CC reduction. Can regulate neurite outgrowth through binding to
CC components of the extracellular matrix such as heparin and
CC collagen I and IV (By similarity). The splice isoforms that
CC contain the BPTI domain possess protease inhibitor activity (By
CC similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis.
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC its serine phosphorylation. Also interacts with GPCR-like protein
CC BPP, FPRL1, APPBP1, TB1, KNS2 (via its TPR domains), APPBP2 (via
CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC MT-binding domains (By similarity). Associates with microtubules
CC in the presence of ATP and in a kinesin-dependent manner (By
CC similarity). Interacts, through a C-terminal domain, with GNAO1
CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein. Cell surface
CC protein that rapidly becomes internalized via clatherin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 95.5%; Score 3485.5; DB 1; Length 770;
Best Local Similarity 87.5%; Pred. No. 2.7e-166;
Matches 674; Conservative 7; Mismatches 14; Indels 75; Gaps 1;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| |||||||||||||||||||||||:||||||||||||:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EPVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTITTTTTESVEEVVR---------- 288

Db        241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTITTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGSVSTQSLLKTTSEPLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345

Db        361 PDKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405

Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465

Db        481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525

Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585

Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645

Db        661 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 7
A4_RAT
ID   A4_RAT          STANDARD;      PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE   amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE   C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE   fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE   Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN   APP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88312583; PubMed=2900758;
RA   Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA   Seeburg P.H.;
RT   "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT   in rat brain suggests a role in cell contact.";
RL   EMBO J. 7:1365-1370(1988).
RN   [2]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89183625; PubMed=2648331;
RA   Kang J., Mueller-Hill B.;
RT   "The sequence of the two extra exons in rat preA4.";
RL   Nucleic Acids Res. 17:2130-2130(1989).
RN   [3]
RP   SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX   PubMed=11483588;
RA   Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT   "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT   family resembling gamma-secretase-like cleavage of Notch.";
RL   J. Biol. Chem. 276:35235-35238(2001).
RN   [4]
RP   ALTERNATIVE SPLICING.
RX   PubMed=8624099;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "APP gene family. Alternative splicing generates functionally related
RT   isoforms.";
RL   Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN   [5]
RP   TISSUE SPECIFICITY OF APPICAN.
RX   PubMed=7744833;
RA   Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA   Mytilineou C., Margolis R.U., Robakis N.K.;
RT   "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT   brain and is produced by astrocytes but not by neurons in primary
RT   neural cultures.";
RL   J. Biol. Chem. 270:11839-11844(1995).
RN   [6]
RP   TISSUE SPECIFICITY OF ISOFORMS.
RX   PubMed=8996834;
RA   Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT   "Expression of the APP gene family in brain cells, brain development
RT   and aging.";
RL   Gerontology 43:119-131(1997).
RN   [7]
RP   INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP   TYR-762.
RX   PubMed=9930726;
RA   Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA   Suzuki T., Nairn A.C., Greengard P.;
RT   "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT   Alzheimer's amyloid precursor protein.";
RL   J. Neurochem. 72:549-556(1999).
RN   [8]
RP   INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND HIS-733.
RX   PubMed=10024358;
RA   Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA   Valenza C., Prochiantz A., Allinquant B.;
RT   "The amyloid precursor protein interacts with Go heterotrimeric
RT   protein within a cell compartment specialized in signal
RT   transduction.";
RL   J. Neurosci. 19:1717-1727(1999).
RN   [9]
RP   CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX   MEDLINE=95256193; PubMed=7737970;
RA   Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT   "The chondroitin sulfate attachment site of appican is formed by
RT   splicing out exon 15 of the amyloid precursor gene.";
RL   J. Biol. Chem. 270:10388-10391(1995).
RN   [10]
RP   BETA-AMYLOID METAL-BINDING.
RX   PubMed=10386999;
RA   Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA   Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA   Bush A.I.;
RT   "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT   peroxide through metal ion reduction.";
RL   Biochemistry 38:7609-7616(1999).
RN   [11]
RP   BETA-AMYLOID ZINC BINDING.
RX   MEDLINE=99343552; PubMed=10413512;
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RA   Liu S.T., Howlett G., Barrow C.J.;
RT   "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT   of the A beta peptide of Alzheimer's disease.";
RL   Biochemistry 38:9373-9378(1999).
RN   [12]
RP   IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP   GLY-704.
RX   PubMed=11959460;
RA   Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT   "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT   peptide 1-42-associated oxidative stress and neurotoxicity.";
RL   Biochim. Biophys. Acta 1586:190-198(2001).
RN   [13]
RP   PHOSPHORYLATION.
RX   PubMed=9085254;
RA   Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA   Greengard P., Suzuki T.;
RT   "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT   phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT   cultured cells.";
RL   Mol. Med. 3:111-123(1997).
RN   [14]
RP   PHOSPHORYLATION ON SER-730.
RX   PubMed=10329382;
RA   Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA   Greengard P., Nairn A.C., Suzuki T.;
RT   "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT   precursor protein at Ser655 by a novel protein kinase.";
RL   Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN   [15]
RP   PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP   THR-743.
RX   MEDLINE=99274744; PubMed=10341243;
RA   Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA   Kirino Y., Greengard P., Suzuki T.;
RT   "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT   during neuronal differentiation.";
RL   J. Neurosci. 19:4421-4427(1999).
RN   [16]
RP   PHOSPHORYLATION ON THR-743.
RX   PubMed=10936190;
RA   Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA   Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT   "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT   protein by cyclin-dependent kinase 5.";
RL   J. Neurochem. 75:1085-1091(2000).
RN   [17]
RP   CARBOHYDRATE STRUCTURE OF APPICAN.
RX   PubMed=11479316;
RA   Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA   Sugahara K., Robakis N.K.;
RT   "Appican, the proteoglycan form of the amyloid precursor protein,
RT   contains chondroitin sulfate E in the repeating disaccharide region
RT   and 4-O-sulfated galactose in the linkage region.";
RL   J. Biol. Chem. 276:37155-37160(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC       G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC       mediating the axonal transport of beta-secretase and presenilin 1
CC       (By similarity). May be involved in copper homeostasis/oxidative
CC       stress through copper ion reduction. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I and IV (By similarity). The
CC       splice isoforms that contain the BPTI domain possess protease
CC       inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain.
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity). Interacts,
CC       through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC       CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC       associates with HADH2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
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  Query Match             95.5%;  Score 3485.5;  DB 1;  Length 770;
  Best Local Similarity   87.4%;  Pred. No. 2.7e-166;
  Matches  673;  Conservative    9;  Mismatches   13;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              || ||:||||||| ||||||||||||||:||||||||||:||||||||||:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |'||||||||||||||||||||||||||||||||||||| | |||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||'|:::||||||||||||||||||||||| |||| ||||||||||:|||
Db        181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              |:|||  ||| :|||||||||||||||||||||||||:|||||||
Db        241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVSSQSLLKTTSEPLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
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Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645

Db        661 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770


RESULT 8
APP2_MOUSE
ID   APP2_MOUSE     STANDARD;      PRT;   695 AA.
AC   Q06335;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).
GN   APLP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RA   von der Kammer H.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-246 FROM N.A.
RX   MEDLINE=94032480; PubMed=8218408;
RA   Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;
RT   "The complete cDNA coding sequence for the mouse CDEI binding
RT   protein.";
RL   Biochim. Biophys. Acta 1216:154-156(1993).
RN   [3]
RP   SEQUENCE OF 185-695 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Heart;
RX   MEDLINE=93129193; PubMed=1482349;
RA   Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
RT   "A murine sequence-specific DNA binding protein shows extensive local
RT   similarities to the amyloid precursor protein.";
RL   Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
RN   [4]
RP   SEQUENCE OF 1-35 FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=96029629; PubMed=7592716;
RA   von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
RA   Gilbert D.J., Jenkins N.A., Sisodia S.S.;
RT   "The mouse APLP2 gene. Chromosomal localization and promoter
RT   characterization.";
RL   J. Biol. Chem. 270:25475-25480(1995).
CC   -!- FUNCTION: BINDS TO THE DNA 5'-GTCACATG-3'(CDEI BOX) WHICH PLAYS
CC       AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC       (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z22592; CAA80306.1; -.
DR   EMBL; M97216; AAA20039.1; -.
DR   EMBL; U34291; AAC52318.1; -.
DR   PIR; S38344; S38344.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88047; Aplp2.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Transmembrane; DNA-binding; Signal; Nuclear protein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    695       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    624       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    625    648       POTENTIAL.
FT   DOMAIN      649    695       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    294       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      218    231       POLY-GLU.
FT   DOMAIN      256    266       POLY-GLU.
FT   CARBOHYD    485    485       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    185    189       GMLLP -> MACCC (1N REF. 3).
SQ   SEQUENCE   695 AA;  78944 MW;  8BF4B95AAB2A0311 CRC64;

  Query Match           47.4%;  Score 1730;  DB 1;  Length 695;
  Best Local Similarity 49.0%;  Pred. No. 4.2e-79;
  Matches  358;  Conservative  119;  Mismatches  163;  Indels   90;  Gaps   19;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56

Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116

Db         75 TGTKSCLGTKEEVILQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176

Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE---E 231

Db        193 DQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEFPTE 243

Qy        232 EEVAEVEEEEEAD-DDEDDEDGDEVEEEAE--------EPYEEATERTTSIATTITTTTES 282

Db        244 ADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTISDKE 301

Qy        283 VEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAE 342

Db        302 IVHDVKVPPTPLPTND-VDVYLETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAE 360

Qy        343 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYI 402

Db        361 LQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYL 420

Qy        403 TALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 462

Db        421 AALQSDPPRPRHILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVI 480

Qy        463 YERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSL 522

Db        481 EERRNQSLTLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSSI 523

Qy        523 TETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSG 582

Db        524 SENPVDVRVSSEFSE-EIPPFHPLHPF-----PSLSENF----------GSGMAEQDG-G 566

Qy        583 LTNIKTEEISEVN-LDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NK 624

Db        567 LIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFSLSS 624

Qy        625 GAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYEN 684

Db        625 NALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYEN 684

Qy        685 PTYKFFEQMQ 694
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                    ||||: ||||
Db          685 PTYKYLEQMQ 694


RESULT 9
APP2_HUMAN
ID   APP2_HUMAN      STANDARD;      PRT;   763 AA.
AC   Q06481;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE   (CDEI-box binding protein) (CDEBP).
GN   APLP2 OR APPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=93250009; PubMed=8485127;
RA   Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA   Norris K., Foster D.C.;
RT   "Molecular cloning of the cDNA for a human amyloid precursor protein
RT   homolog: evidence for a multigene family.";
RL   Biochemistry 32:4481-4486(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=95217334; PubMed=7702756;
RA   von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
RT   "A human amyloid precursor-like protein is highly homologous to a
RT   mouse sequence-specific DNA-binding protein.";
RL   DNA Cell Biol. 13:1137-1143(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94035131; PubMed=8220435;
RA   Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA   Hyman B.T., Neve R.L., Tanzi R.E.;
RT   "Isolation and characterization of APLP2 encoding a homologue of the
RT   Alzheimer's associated amyloid beta protein precursor.";
RL   Nat. Genet. 5:95-99(1993).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC       SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC       FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC       MAY BIND TO THE DNA 5'-GTCACATG-3'(CDEI BOX).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC       (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=Q06481-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q06481-2; Sequence=VSP_000018;
CC       Name=3;
CC         IsoId=Q06481-3; Sequence=VSP_000019;
CC   -!- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
CC       AND ENDOTHELIAL TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S60099; AAC60589.1; -.
DR   EMBL; L09209; AAA35526.1; -.
DR   EMBL; Z22572; CAA80295.1; -.
DR   EMBL; L27631; AAC41701.1; -.
DR   EMBL; BC000373; AAH00373.1; -.
DR   PIR; A49321; A49321.
DR   HSSP; P05067; 1MWP.
DR   Genew; HGNC:598; APLP2.
DR   MIM; 104776; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0003677; F:DNA binding activity; NAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Signal; Alternative splicing; DNA-binding;
KW   Nuclear protein; Serine protease inhibitor.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    763       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    692       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    693    716       POTENTIAL.
FT   DOMAIN      717    763       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      215    280       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      306    364       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      215    231       POLY-GLU.
FT   ACT_SITE    320    321       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    310    360       BY SIMILARITY.
FT   DISULFID    319    343       BY SIMILARITY.
FT   DISULFID    335    356       BY SIMILARITY.
FT   VARSPLIC    308    363       Missing (in isoform 2).
FT                                /FTId=VSP_000018.
FT   VARSPLIC    613    624       Missing (in isoform 3).
FT                                /FTId=VSP_000019.
FT   CONFLICT    543    543       S -> I (IN REF. 1).
SQ   SEQUENCE   763 AA;  86955 MW;  CA3A7D6DDB8A28D0 CRC64;

  Query Match             47.2%;  Score 1725;  DB 1;  Length 763;
  Best Local Similarity   46.9%;  Pred. No. 8.4e-79;
  Matches  369;  Conservative  112;  Mismatches  170;  Indels  136;  Gaps   19;
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RESULT 10
APP2_RAT
ID   APP2_RAT       STANDARD;      PRT;   765 AA.
AC   P15943;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
GN   APLP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-627 FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain, and Heart;
RX   MEDLINE=94368849; PubMed=8086458;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT   protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT   difference to human and murine homologues.";
RL   Biochim. Biophys. Acta 1219:167-170(1994).
RN   [2]
RP   SEQUENCE OF 575-765 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=90207205; PubMed=1690887;
RA   Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT   "Characterization of cDNA encoding a human sperm membrane protein
RT   related to A4 amyloid protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=P15943-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=P15943-2; Sequence=VSP_000021;
CC       Name=C;
CC         IsoId=P15943-3; Sequence=VSP_000020;
CC       Name=D;
CC         IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X77934; CAA54906.1; -.
DR   EMBL; M31322; AAA42352.1; -.
DR   PIR; A35981; A35981.
DR   PIR; S42880; S42880.
DR   HSSP; P05067; 1MWP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPII; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Alternative splicing; Serine protease inhibitor;
KW   Signal; Glycoprotein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    765       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    695       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    696    718       POTENTIAL.
FT   DOMAIN      719    765       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    282       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      308    366       BPTI/KUNITZ INHIBITOR.
FT   ACT_SITE    322    323       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    312    362       BY SIMILARITY.
FT   DISULFID    321    345       BY SIMILARITY.
FT   DISULFID    337    358       BY SIMILARITY.
FT   DOMAIN      218    229       POLY-GLU.
FT   CARBOHYD    628    628       O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT   VARSPLIC    311    365       Missing (in isoform C and isoform D).
FT                                /FTId=VSP_000020.
FT   VARSPLIC    616    627       Missing (in isoform B and isoform D).
```

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FT                                 /FTId=VSP_000021.
FT   CONFLICT    575    577        DQF -> EFV (IN REF. 2).
SQ   SEQUENCE   765 AA;  86682 MW;  CF51FCCCE305ACCF CRC64;

  Query Match              46.8%;  Score 1709;  DB 1;  Length 765;
  Best Local Similarity    45.9%;  Pred. No. 5.2e-78;
  Matches  361;  Conservative  124;  Mismatches  168;  Indels  134;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
                :|||   || |             |:|    :||||:||||:'|||:|:| ||:: |:
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :|||||:||||||.||:|||||| | :||:| :|||::  | |||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||||||| |||:: |:| ||||:||| |   |||  :| |  :     :: |||..|||:
Db        133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYA-DGSEDKVVEVAEEEE 233
              |:| | |:|||| :  :||: : : ||:: :       : |:| | |:        |:
Db        193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEE----DEEEDYALDKSEFPTEADLEDFT 248

Qy        234 VAEVEEEEADDDEDDEDGDEVEEEAEEPYEE------ATERTTSIATTTTTTTESVEEVV 287
                | :|:| :::|::|::|:|:|                 |   |    :   :     |
Db        249 EAAADEDEDEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV 308

Qy        288 R--------------------------------------------------------VPT 291
              :                                                          :|
Db        309 KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMIPP 368

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
              |  ' | ||  ||  :||||| ||||||:|| :|'  | :| :||||:  ||||:|||
Db        369 TPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRSRMDRVKKEWEEAELQAKNLPKA 427

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
              ::: :|:||| :::||:|||:|:| |||:: ||||..|||||:||||:: |||: |||
Db        428 ERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYLAALQSDPPR 487

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
              |  :   |::|||:| ||| |::|::::|  |:'|:||::||||'|| '. || |||
Db        488 PHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSLS 547

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
              ||| :| ||:||||:|:||||:::               ::             |::|    :
Db        548 LLYKVPYVAQEIQEEIDELLQEQR-------ADM---------DQFTSSISENPVDVR- 589

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARP------AADRGLTTRPGSGLTN 585
                 |: | | ::: ::| |       |: :|||     | :|          |:  : | .
Db        590 --VSSEES-EEIPPFHPF--HPFPSLSENE----DTQPELYHPMKKGSGMAEQDG-GLIG 639

Qy        586 IKTEEISEVN-LDAEFRHDSGYEVHHQKLVFFAEDVGS-----------------NKGAI 627
                : : |:  | :|     |     | :| ::::| |: ||                 : |:
Db        640 AEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPDSVGPLREDFSLSSSAL 697

Qy        628 IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTY 687
              :||:|  |||||||||:|||||:|:||:|  :|:|||    :||||:|| ||:||| |||||
Db        698 IGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPMLTPEERHLNKMQNHGYENPTY 757

Qy        688 KFFEQMQ 694
              |: ||||
Db        758 KYLEQMQ 764


RESULT 11
APP1_HUMAN
ID   APP1_HUMAN     STANDARD;      PRT;   650 AA.
AC   P51693; Q00113; Q96A92;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN   APLP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98088960; PubMed=9428684;
RA   Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L., Multhaup G.,
RA   Masters C.L., Beyreuther K., Weidemann A.;
RT   "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
RT   expression in COS-7 cells and identification of soluble forms in the
RT   cerebrospinal fluid.";
RL   Eur. J. Biochem. 250:354-363(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98180887; PubMed=9521588;
RA   Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
RA   Olsen A., Tryggvason K.;
RT   "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT   19q13.1.";
RL   Hum. Genet. 102:192-196(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
RX   MEDLINE=96115107; PubMed=7494461;
RA   Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
RA   Black I.B.;
RT   "Selective localization of amyloid precursor-like protein 1 in the
RT   cerebral cortex postsynaptic density.";
RL   Brain Res. Mol. Brain Res. 32:36-44(1995).
RN   [5]
RP   HEPARIN AND ZINC BINDING.
RX   MEDLINE=95014513; PubMed=7929392;
RA   Bush A.I., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RT   "The amyloid beta-protein precursor and its mammalian homologues.
RT   Evidence for a zinc-modulated heparin-binding superfamily.";
RL   J. Biol. Chem. 269:26618-26621(1994).
RN   [6]
RP   INTERACTION WITH APBA2.
RX   MEDLINE=99107877; PubMed=9890987;
RA   Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA   Sakiyama S., Kirino Y., Suzuki T.;
RT   "Interaction of a neuron-specific protein containing PDZ domains with
RT   Alzheimer's amyloid precursor protein.";
RL   J. Biol. Chem. 274:2243-2254(1999).
RN   [7]
RP   EXTRACELLULAR COPPER-BINDING.
RX   MEDLINE=22130992; PubMed=12135352;
RA   Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,
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RA   Reed J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
RA   Bayer T.A., Multhaup G.;
RT   "Evidence for a copper-binding superfamily of the amyloid precursor
RT   protein.";
RL   Biochemistry 41:9310-9320(2000).
CC   -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC       gamma-secretase processed fragment, AL1D1, activates transcription
CC       activation through APBB1 (Fe65) binding (By similarity). Couples
CC       to JIP signal transduction through C-terminal binding. May
CC       interact with cellular G-protein signaling pathways. Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I.
CC   -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC       neuronal apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB and APBA family members,
CC       MAPK8IP1 and Dabl (By similarity). Binding to Dabl inhibits its
CC       serine phosphorylation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC       processed in the Golgi complex.
CC   -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
CC       localized to the postsynaptic density (PSD).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The NPXY site is also involved in clatherin-mediated
CC       endocytosis.
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal
CC       apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
CC       similarity).
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: O-glycosylated.
CC   -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC       Zinc-binding increases heparin binding. No Cu(II) reducing
CC       activity with copper-binding.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U48437; AAB96331.1; -.
DR   EMBL; AD000864; AAB50173.1; -.
DR   EMBL; BC012889; AAH12889.1; -.
DR   HSSP; P05067; 1MWP.
DR   Genew; HGNC:597; APLP1.
DR   MIM; 104775; -.
DR   GO; GO:0005604; C:basement membrane; TAS.
DR   GO; GO:0005208; F:amyloid protein; TAS.
DR   GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR   GO; GO:0007399; P:neurogenesis; TAS.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW   Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW   Glycoprotein.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    650       AMYLOID-LIKE PROTEIN 1.
FT   CHAIN       621    650       C30 (BY SIMILARITY).
FT   DOMAIN       39    580       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    581    603       POTENTIAL.
FT   DOMAIN      604    650       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      158    178       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      204    211       ZINC-BINDING.
FT   DOMAIN      310    342       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      410    441       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      442    459       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      640    643       CLATHRIN-BINDING (POTENTIAL).
FT   DOMAIN      241    247       POLY-GLU.
FT   DOMAIN      264    268       POLY-GLU.
FT   SITE        167    167       REQUIRED FOR COPPER(II) REDUCTION (BY
FT                                SIMILARITY).
FT   SITE        604    615       BASOLATERAL SORTING SIGNAL (BY
FT                                SIMILARITY).
FT   SITE        620    621       CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT   SITE        638    641       ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT   SITE        640    643       NPXY MOTIF.
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    461    461       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    551    551       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     48     48       A -> P (IN REF. 1).
SQ   SEQUENCE   650 AA;  72176 MW;  B95F0F4D1C5CBAC7 CRC64;

  Query Match             32.6%;  Score 1191;  DB 1;  Length 650;
  Best Local Similarity   38.4%;  Pred. No. 2.4e-52;
  Matches  271;  Conservative  121;  Mismatches  221;  Indels   92;  Gaps   16;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              :|| | ||| |     :|   : | |      |:|  |||| :| ::: |:|: ||  ::
Db         23 LLPLLLLLLRAQPAIGSLAGGSPGAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRSR 82

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCLV 119
               |:   : :|:||:::|||||  | :| | : :: :|   |     ||:  |:|:|||
Db         83 RCLRDPQRVLEYCRQMYPELQIARVEQATQAIPMERWCGGSRSGSCAHPHHQVVPFRCLP 142

Qy        120 GEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKF 179
              |||||:|||||: .:|||:|||| ||:    | |:| || :   ||  |||:|||| |:|
Db        143 GEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDRF 202

Qy        180 RGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEE 239
              ||||:|||     |   | | |  |  |          ||    || ||:||    ||
Db        203 RGVEYVCCPPPGTPD--PSGTAVGDPSTRSW-------PPGSR---VEGAEDEE----EE 246

Qy        240 EEADDDEDD--EDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
              |     ||   :  : ||| ||     :  | ::   | |           ||
Db        247 ESFPQPVDDYFVEPPQAEEE-EETVPPPSSHTLAVVGKVTPTPR--------PT------ 291

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHREKMSQVMREWEEAERQAKNLPKADKKAVI 357
              | || |   ||: :|:  | :||  || :   :::|||||  |: |:|:||||||::|:
Db        292 DGVDIYPGMPGEISEHEGFLRAKMDLEERRMRQINEVMREWAMADNQSKNLPKADRQALN 351

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              :|||  :::||:: : |||:|||||  || |::||:|| ||| :: |||| ||:   |
Db        352 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQADPPQAERVLL 411

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |::|:|||||:::|||:|::||  |||:|| |:: || |||:|| ||:|||| ||   |
Db        412 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVHTHLQVIEERVNQSLGLLDQNP 471

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLIETKTTVELLPVNGE 537
              :|:|:: :: |||  |                     ) ||  |       | |
Db        472 HLAQELRPQIQELLHSEH--------------------LGPSELEA-------PAPGG 502

Qy        538 FSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLD 597
              | |                 :  ::| |::   |  :|   ||   :  : |  ::|
Db        503 SSED----------------KGGLQPPDSKD--DTPMILPKGSIEQDAASPEKEKMNPL 543

Qy        598 AEFRH------DSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML 648
              ::          |:  |    |:         | :: |: |::: |    ::|:::::|
Db        544 EQYERKVNASVPRGFPFHSSEIQRDELAPAGTGVSREAVSGLLIMGAGGGSLIVLSMLLL 603

Qy        649 -KKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPIYKFFEQ 692
              :|| | :| |||||||  :| |: | ::|::|||||||:| |:
Db        604 RRKKPYGAISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 648


RESULT 12
```

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APP1_MOUSE
ID   APP1_MOUSE     STANDARD;      PRT:   653 AA.
AC   Q03157; Q8VC38;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 1 precursor (APLP) (APLP-1) (Contains: C30).
GN   APLP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=93056322; PubMed=1279693;
RA   Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
RA   Solomon F.;
RT   "Identification of a mouse brain cDNA that encodes a protein related
RT   to the Alzheimer disease-associated amyloid beta protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   COLLAGEN-BINDING.
RX   MEDLINE=96139497; PubMed=8576160;
RA   Beher D., Hesse L., Masters C.L., Multhaup G.;
RT   "Regulation of amyloid protein precursor (APP) binding to collagen and
RT   mapping of the binding sites on APP and collagen type I.";
RL   J. Biol. Chem. 271:1613-1620(1996).
RN   [4]
RP   INTERACTION WITH DAB1.
RX   MEDLINE=99388880; PubMed=10460257;
RA   Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT   "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RT   protein 1.";
RL   J. Neurosci. 19:7507-7515(1999).
RN   [5]
RP   INTERACTION WITH MAPK8IP1.
RX   MEDLINE=21408156; PubMed=11517249;
RA   Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA   Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA   Kyriakis J.M., Nishimoto I.;
RT   "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT   scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL   J. Neurosci. 21:6597-6607(2001).
RN   [6]
RP   GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
RP   TYR-641.
RX   MEDLINE=22313598; PubMed=12228233;
RA   Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
RT   "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RT   secretase regulates transcription.";
RL   J. Biol. Chem. 277:44195-44201(2002).
CC   -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC       gamma-secretase processed fragment, ALID1, activates transcription
CC       activation through APBB1 (Fe65) binding. Couples to JIP signal
CC       transduction through C-terminal binding. May interact with
CC       cellular G-protein signaling pathways. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I.
CC   -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC       neuronal apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB and APBA family members,
CC       MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC       serine phosphorylation.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC       processed in the Golgi complex.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The NPXY site is also involved in clatherin-mediated
CC       endocytosis.
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal
CC       apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC       similarity).
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: O-glycosylated.
CC   -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC       Zinc-binding increases heparin binding. No Cu(II) reducing
CC       activity with copper-binding.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L04538; AAA37247.1; -.
DR   EMBL; BC021877; AAH21877.1; -.
DR   PIR; A46362; A46362.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88046; Aplp1.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW   Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW   Glycoprotein.
FT   SIGNAL       1     37       POTENTIAL.
FT   CHAIN       38    653       AMYLOID-LIKE PROTEIN 1.
FT   CHAIN      624    653       C30 (BY SIMILARITY).
FT   DOMAIN      38    583       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   584    606       POTENTIAL.
FT   DOMAIN     607    653       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     157    177       COPPER-BINDING.
FT   DOMAIN     203    210       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN     313    345       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     413    444       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     445    462       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN     263    271       POLY-GLU.
FT   DOMAIN     535    538       POLY-SER.
FT   DOMAIN     601    606       POLY-LEU.
FT   SITE       166    166       REQUIRED FOR COPPER(II) REDUCTION (BY
FT                               SIMILARITY).
FT   SITE       607    618       BASOLATERAL SORTING SIGNAL (BY
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FT                                   SIMILARITY).
FT   SITE         623    624         CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT   SITE         641    644         ENDOCYTOSIS SIGNAL.
FT   SITE         643    646         NPXY MOTIF.
FT   CARBOHYD     464    464         N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     554    554         N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MUTAGEN      641    641         Y->G: REDUCED BINDING OF APBB1.
FT   CONFLICT      17     17         P -> PP (IN REF. 2).
SQ   SEQUENCE   653 AA;  72750 MW;  56516DC3EA40E4B0 CRC64;

  Query Match             32.4%;  Score 1183;  DB 1;  Length 653;
  Best Local Similarity   39.0%;  Pred. No. 5.9e-52;
  Matches  275;  Conservative  121;  Mismatches  221;  Indels   88;  Gaps   20;

Qy          1 MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGT 59
Db         22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy         60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
Db         81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAIPMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy        119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
Db        141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDR 200

Qy        179 FRGVEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
Db        201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-------EEEVESF 246

Qy        238 EEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
Db        249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR--------PT------ 294

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
Db        295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
Db        355 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
Db        415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
Db        475 HLAQELRPQIQELL----------LAEHLGPSEL----DASVPGSSSEDK---------- 510

Qy        537 EFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSG-----LTNIKTEEI 591
Db        511 ----GSLQP-------------PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYE- 550

Qy        592 SEVNLDAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML 648
Db        551 QKVNASA----PRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSLIVLSLLLL 606

Qy        649 -KKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
Db        607 RKKKPYGTISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 651

RESULT 13
A4_CAEEL
ID   A4_CAEEL       STANDARD;      PRT;   686 AA.
AC   Q10651; Q18583; Q95ZX1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-amyloid-like protein precursor.
GN   APL-1 OR C42D8.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE OF 6-686 FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=94089766; PubMed=8265668;
RA   Daigle I., Li C.;
RT   "apl-1, a Caenorhabditis elegans gene encoding a protein related to
RT   the human beta-amyloid protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:12045-12049(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Hallsworth K.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   REVISIONS, AND ALTERNATIVE SPLICING.
RA   Waterston R.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=a;
CC         IsoId=Q10651-1; Sequence=Displayed;
CC       Name=b;
CC         IsoId=Q10651-2; Sequence=VSP_000017;
CC         Note=No experimental confirmation available;
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U00240; AAC46470.1; ALT_INIT.
DR   EMBL; U56966; AAA98722.1; -.
DR   EMBL; U56966; AAK68242.1; -.
DR   PIR; T15795; T15795.
DR   HSSP; P05067; 1MWP.
DR   WormPep; C42D8.8a; CE04209.
DR   WormPep; C42D8.8b; CE27845.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
KW   Signal; Transmembrane; Amyloid; Neurogenesis; Glycoprotein;
KW   Alternative splicing.
FT   SIGNAL         1     21       POTENTIAL.
FT   CHAIN         22    686       BETA-AMYLOID-LIKE PROTEIN.
FT   DOMAIN        22    621       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     622    642       POTENTIAL.
FT   DOMAIN       643    686       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       205    228       ASP-RICH.
FT   DOMAIN       676    679       CLATHRIN-BINDING (POTENTIAL).
FT   CARBOHYD      84     84       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     249    249       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     538    539       Missing (in isoform b).
FT                                 /FTId=VSP_000017.
SQ   SEQUENCE   686 AA;  79434 MW;  A0816858FDD48608 CRC64;

  Query Match             22.3%;  Score 815.5;  DB 1;  Length 686;
  Best Local Similarity   29.1%;  Pred. No. 1.2e-33;
  Matches  222;  Conservative  109;  Mismatches  276;  Indels  155;  Gaps   22;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          6 LMIGLLIPILVA-IVYAEGSPAGSKRHEKFIPMVAFSCQYRNQYM-IEEGSWKTDDERYA 63

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVIIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||   |  ||:|!:: || : |||:|: :  |:| :|||:     ||   | | || ': |
Db         64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN------LHDYGMLLPC 174
              :| |:|| ||  |:: |    | |  : ||   | : |  : :       :  : :, ||
Db        123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy        175 GIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEV 234
              :| | ||||||||    :|  :  | ::
Db        183 ALDMFTGVEFVCCP----NDQTNKTDVQKIK---------------------------- 209

Qy        235 AEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAA 294
                 |:|: ||||||   |:  ||:::  ||
Db        210 ---EDEDDDDDEDDAYEDDYSEESDEKDEE---------------------------- 236

Qy        295 STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA-----ERQAKNLP 349
              | : | | :     |||  |:||: |:: ||||:: :|||:|| :      |:::|: !
Db        237 -EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHRKKVDKVMKEWGDLETRYNEQKAKD-P 294

Qy        350 KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL- 405
              |  :|   |    ||: ' |||:|    |:::   |  ||:|||.::::| |  :|  ||
Db        295 KGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA 354

Qy        406 -QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE 464
                 !    |   || |:|||:||| |||  : |:   ; |:||  :  |:  :| |
Db        355 THVNKPNKHSVLQSLKAYIRAEEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL 414

Qy        465 RMNQSLSLLYNVP---------AVA--EEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
              |:| :|:::| : |         ||   :: :'|:   :  |       |  :| :  |
Db        415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE----DSELTPIIHDDEFSK 470

Qy        514 GN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANT---ENEVEP 564
                 |    : |    :     ::||     | ::   ::    |           : : :
Db        471 NAKLDVKAPTTTAKPVKETDNAKVLPTEASDSEEEADEYYEDEDDEQVKKTPDMKKKVKV 530

Qy        565 VDARP--------------------AADRGLTTRPGSGLTNIKTEE-----ISEVNLDA 598
              |: :|                    !       |  |: :::!     | |: :|
Db        531 VDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSSESDEDEDKNIKELRVDI 590

Qy        599 E---------FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 649
              |         :|||        ||:   ;  !        ::   :  | ! |    :
Db        591 EPIIDEPASFYRHD--------KLIQSPEVERSASSVFQPYVLASAMFITAICIIAFAIT 642

Qy        650 KKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
                :      | :|||   |||:|||:: |. ||||:||| ::
Db        643 NARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFPD 683


RESULT 14
A4_DROME
ID   A4_DROME       STANDARD;      PRT;   887 AA.
AC   P14599; Q9TVV0; Q9U4H3; Q9W5F1;
DT   01-APR-1990 (Rel. 14, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-amyloid-like protein precursor.
GN   APPL OR VND OR BCDNA:GH04413 OR EG:65F1.5 OR CG7727.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89184650; PubMed=2494667;
RA   Rosen D.R., Martin-Morris L., Luo L., White K.;
RT   "A Drosophila gene encoding a protein resembling the human
RT   beta-amyloid protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [3]
RP   REVISIONS.
RC   STRAIN=Berkeley;
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Oregon-R;
RX   MEDLINE=20196011; PubMed=10731137;
RA   Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA   Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA   Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA   Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA   Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA   Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
RA   Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
RA   Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA   McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA   Glover D.M.;
RT   "From sequence to chromosome: the tip of the X chromosome of D.
RT   melanogaster.";
RL   Science 287:2220-2222(2000).
RN   [5]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley; TISSUE=Ovary;
RX   MEDLINE=20196012; PubMed=10731138;
RA   Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
RA   Stapleton M., Harvey D.A.;
RT   "A Drosophila complementary DNA resource.";
RL   Science 287:2222-2224(2000).
RN   [6]
RP   SEQUENCE OF 1-83 FROM N.A.
RX   MEDLINE=91184006; PubMed=2127912;
RA   Martin-Morris L.E., White K.;
RT   "The Drosophila transcript encoded by the beta-amyloid protein
RT   precursor-like gene is restricted to the nervous system.";
RL   Development 110:185-195(1990).
CC   -!- FUNCTION: Probably corresponds to the protein encoded by the
CC       essential locus vnd, a gene required for embryonic nervous system
CC       development.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in post-mitotic neurons in the
CC       central and peripheral nervous systems. Within the nervous system
CC       transcripts are not observed in neuroblasts, newly generated
CC       neurons and at least one class of presumed glial cells.
CC   -!- DEVELOPMENTAL STAGE: Expressed in all developmental stages.
CC   -!- DOMAIN: The clathrin-binding site is essential for its association
CC       with x11-alpha, -beta, and -gamma. The sequence specific
CC       recognition extends to peptide residues that are C-terminal to the
CC       NPXY motif. This interaction appears to be independent of
CC       phosphorylation (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J04516; AAA28874.1; -.
DR   EMBL; AE003418; AAF45520.2; -.
DR   EMBL; AL031883; CAA21409.1; -.
DR   EMBL; AL022139; CAA21409.1; JOINED.
DR   EMBL; AL022139; CAA18093.1; -.
DR   EMBL; AL031883; CAA18093.1; JOINED.
DR   EMBL; AF181628; AAD55414.1; -.
DR   EMBL; X55774; CAA39294.1; -.
DR   EMBL; X55775; CAA39294.1; JOINED.
DR   PIR; A32758; A32758.
DR   HSSP; P05067; 1MWP.
DR   FlyBase; FBgn0000108; Appl.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal; Transmembrane; Amyloid; Neurogenesis.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    887       BETA-AMYLOID-LIKE PROTEIN.
FT   DOMAIN       28    813       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    814    834       POTENTIAL.
FT   DOMAIN      835    887       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      877    880       CLATHRIN-BINDING (POTENTIAL).
FT   CARBOHYD    150    150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    237    237       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    240    240       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    574    574       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    177    177       S -> T (IN REF. 1).
FT   CONFLICT    229    229       MISSING (IN REF. 1).
FT   CONFLICT    332    332       V -> M (IN REF. 4).
FT   CONFLICT    743    743       S -> T (IN REF. 1).

SQ   SEQUENCE   887 AA;  98332 MW;  F0F0855AD65A5275 CRC64;

  Query Match           20.5%;  Score 747.5;  DB 1;  Length 887;
  Best Local Similarity   25.5%;  Pred. No. 3.8e-30;
  Matches  233;  Conservative  127;  Mismatches  288;  Indels  265;  Gaps   29;

Qy          7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDSDPSG 58
              ||| : |   |:      | | : |     ||||||: |  |::      : : |:| :| |
Db          9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVIDLSK 63

Qy         59 T---KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
                 ||:  |  :| |||:: ||   |||:|||::    |  |||:|     :||    ::
Db         64 KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWI 123

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
              |:||| | | .||||||: | | |       |   : |:       | |:   :  : |||
Db        124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRSFAMLL 182

Qy        173 PCGIDKFRGVEFVCCP-----------------------------LAEESDNVD---S 198
              ||||  | ||||||||                             : :: |: |   |
Db        183 PCGISVFSGVEFVCCPKHFKTDEIHVKKTDLPVMPAAQINSANDELVMNDEDDSNDSNYS 242

Qy        199 ADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV----------------------AE 236
              || ||| |      | |   | :::   ||:|                          ||
Db        243 KDANEDDLD------DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINAE 296

Qy        237 VEE-EEADDDEDDEDGDEVEEEAEEPY--------------------------EEATER 268
              :  || |: |:|  ' | | | ! |  :                          |:|  :
Db        297 YDSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLKSDSSSPSSAPVAPAPEKAPVK 356

Qy        269 TTSIATTTTTTTTESVEEVV----------RVPTTAASTPDAVDKYLETPGDENEHAHFQ 317
              : |: :|   :  :   |              |:'|  |    | |        ||  ::
Db        357 SESVTSTPQLSASAAAFVAANSGNSGTGAGAPPSTAQPTS---DPYFTHFDPHYEHQSYK 413

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKA-------VIQHFQEKVESLEQE 370
              :::|||  |||:::::||:|: | | : :::  || ||       :   ||  |::||:|
Db        414 VSQKRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFKQRMTARFQTSVQALEEE 473

Qy        371 AANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDR 430
              |: '|  :  || | :| |:| |:  |  ||   ||   ||   |:| :|'  |||
Db        474 GNAEKHQLAAMHQQRVLAHINQRKREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDR 533

Qy        431 QHTLKHFEH-VRMVDP---KKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI--- 483
              | | |: | :    |   : ||  | : :  | |   :|||:::|   | : :!
Db        534 AHALAHYRHLLNSGGPGGLEAAASERPRTLERLIDIDRAVNQSMTMLKRYPELSAKIAQL 593

Qy        484 ----------QDEV---------------------------------------------- 487
                       :;::
Db        594 MNDYILALRSKDDIPGSSLGMSEEAEAGILDKYRVEIERKVAEKERLRLAEKQRKEQRAA 653

Qy        488 ------DELLQKEQNYSDDVLANMISE----------------------PRISYGNDAL 518
                   :| |: |   ||:| : ::|                        |   | ||
Db        654 EREKLREEKLRLEAKKVDDMLKSQVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAA 713

Qy        519 M-----PSLIETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADR 573
              :     |:|  ||:          |  | | :    :|  :| :     | |     |  |
Db        714 LVTAANPNLETTKS---------EKDLSDTE----YGEATVSSTKVQTVLPTVDDDAVQR 760

Qy        574 GLITRPGSGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---G 625
              :     :      ::   : : :|   ::: |:: |     ||:   : |
Db        761 AVEDVAAA---------VAHQEAEPQVQHFMTHDLGHRESSFSLRREFAQHAHAAKEGRN 811

Qy        626 AIIGLMVGGVVIATVIVITLVMLKKKQYTSIH-HGVVEVDAAVTP------EERHLSKMQ 678
              |   |: :   : : : : : :   | |  | :|||  ||       ||: :  ||
Db        812 VYFTLSFAGIALMAAVFVGVAVAKWRTSRSPHAQGFIEVDQNVTTHHPIVREEKIVPNMQ 871

Qy        679 QNGYENPTYKFFE 691
               ||||:|||| :||
Db        872 INGYENPTYKYFE 884


RESULT 15
A4_BOVIN
```

```
ID   A4_BOVIN        STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; PC5067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             7.8%;  Score 284;  DB 1;  Length 59;
  Best Local Similarity   96.6%;  Pred. No. 1.5e-05;
  Matches   57;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        591 ISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 649
              |||| :|||||||||||||||||||||||||||||||||||| |||| |||||| ||||
Db          1 ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 59


Search completed: October 2, 2003, 13:59:39
Job time : 14 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:24 ; Search time 39 Seconds
(without alignments)
4611.863 Million cell updates/sec

Title: US-09-806-194-18
Perfect score: 3651
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3565	97.6	695	11	Q60496	Q60496 cavia sp. p
2	3532	96.7	695	11	P97487	P97487 mus musculu
3	3527.5	96.6	770	6	Q9TUI0	Q9tui0 sus scrofa
4	3420	93.7	695	13	Q9DGJ8	Q9dgj8 gallus gall
5	3379	92.5	751	13	Q9DGJ7	Q9dgj7 gallus gall
6	3206	87.8	693	13	Q98SG0	Q98sg0 xenopus lae
7	3182	87.2	695	13	Q98SF9	Q98sf9 xenopus lae
8	3095	84.8	747	13	Q91963	Q91963 xenopus. ap
9	2956.5	81.0	699	13	O57394	O57394 narke japon
10	2759.5	75.6	569	13	Q9PVL1	Q9pvl1 gallus gall
11	2627.5	72.0	607	11	Q99K32	Q99k32 mus musculu
12	2605	71.4	534	13	O93296	O93296 gallus gall
13	2568	70.3	780	13	O73683	O73683 tetraodon f
14	2524	69.1	738	13	Q90W28	Q90w28 brachydanio
15	2487.5	68.1	694	13	Q8UUR9	Q8uur9 brachydanio
16	2446.5	67.0	737	13	O93279	O93279 fugu rubrip
17	2334	63.9	612	13	Q9I9E7	Q9i9e7 brachydanio
18	1920	52.6	384	11	Q8BPC7	Q8bpc7 mus musculu
19	1762	48.3	695	4	Q13861	Q13861 homo sapien
20	1746.5	47.8	669	4	Q14662	Q14662 homo sapien
21	1735	47.5	695	11	Q64348	Q64348 mus musculu
22	1701	46.6	763	11	Q61482	Q61482 mus musculu
23	1699	46.5	751	11	Q60709	Q60709 mus musculu
24	1650	45.2	472	13	Q8UUS0	Q8uus0 brachydanio
25	1345.5	36.9	357	13	Q8UUI8	Q8uui8 brachydanio
26	1301.5	35.6	522	4	Q9BT36	Q9bt36 homo sapien
27	1082	29.6	218	11	Q8BPV5	Q8bpv5 mus musculu
28	1048.5	28.7	523	4	Q14594	Q14594 homo sapien
29	771	21.1	239	13	Q8UUI7	Q8uui7 brachydanio
30	678	18.6	136	6	P79307	P79307 sus scrofa
31	569	15.6	113	13	Q8JH58	Q8jh58 chelydra se
32	561	15.4	182	11	Q9CYS4	Q9cys4 mus musculu
33	478	13.1	97	6	Q28673	Q28673 oryctolagus
34	385.5	10.6	82	4	Q16019	Q16019 homo sapien
35	381.5	10.4	82	4	Q16014	Q16014 homo sapien
36	379.5	10.4	82	4	Q16020	Q16020 homo sapien
37	368	10.1	79	11	O35463	O35463 cricetulus
38	358.5	9.8	160	11	Q9QZ78	Q9qz78 cavia sp. p
39	328	9.0	208	11	Q8R0R7	Q8r0r7 mus musculu
40	239	6.5	49	6	O97917	O97917 bos taurus
41	196.5	5.4	727	5	Q95TG7	Q95tg7 drosophila
42	196.5	5.4	5303	5	Q9V628	Q9v628 drosophila
43	194	5.3	785	5	Q9GQ82	Q9gq82 drosophila
44	192.5	5.3	556	5	Q95S93	Q95s93 drosophila
45	192.5	5.3	1110	13	Q91255	Q91255 petromyzon

ALIGNMENTS

RESULT 1
Q60496
ID Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative amyloid precursor protein.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 97.6%; Score 3565; DB 11; Length 695;
Best Local Similarity 97.6%; Pred. No. 2e-206;
Matches 678; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||  ||||||||||||||||||||||||||:||||||||||: ||||||
Db          1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWEPDPSGTK 60
```

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Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db          61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db         181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db         241 EADDDEDVEDGDEVEEEAEEPYEEATEKTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
Db         541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
```

```
RESULT 2
P97487
ID   P97487     PRELIMINARY;      PRT;   695 AA.
AC   P97487; P97942;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hippocampal amyloid protein.
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RA   Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 581-662 FROM N.A.
RC   STRAIN=129SV;
RA   Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA   Loring J.F., Goate A.M.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U84012; AAB41502.1; -.
DR   EMBL; U82624; AAB40919.1; -.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78414 MW;  9A5FBE2ED261236E CRC64;

  Query Match             96.7%;  Score 3532;  DB 11;  Length 695;
  Best Local Similarity   97.0%;  Pred. No. 1.9e-204;
  Matches  674;  Conservative    6;  Mismatches   15;  Indels    0;  Gaps    0;

Qy           1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db           1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db          61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db         181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db         241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESVEEVVRVPTTAASTPDAA 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600
Db         541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Db         601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

RESULT 3
Q9TUI0
ID   Q9TUI0     PRELIMINARY;      PRT;   770 AA.
AC   Q9TUI0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Amyloid precursor protein.
OS   Sus scrofa (Pig).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid Precursor Protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB032550; BAA84580.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   770 AA;  86961 MW;  5F7A1DCB2BCC583E CRC64;

  Query Match             96.6%;  Score 3527.5;  DB 6;  Length 770;
  Best Local Similarity   88.2%;  Pred. No. 4.1e-204;
  Matches  679;  Conservative    9;  Mismatches    7;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||:|||||||||| ||||||||||||||:||||:||||||||||:||.|||||
Db          1 MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||:|||||||||||||||||| |||'||| | ||||.||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||:|||||||:|||| |||||||:|||| |||,||||..||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||:|||||||||||||||:|||| ||||-|||| |||||||:|  |
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              ||::|||||||||||||||'||||||:|||||| |||| ||||||
Db        241 EAEDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLLKTTQEHLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||||||||||:||||:||||||||||:|||||:|||||:|||||:|||:
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||'|||||||||||||'|||.|||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRKLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||:|||||||||||||| || ||||||||||:|||||'||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              |||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 4
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             93.7%;  Score 3420;  DB 13;  Length 695;
  Best Local Similarity   93.7%;  Pred. No. 1e-197;
  Matches  653;  Conservative   18;  Mismatches   22;  Indels    4;  Gaps    3;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |.| |||||||  |||||| ||||||||||||||||||:||||||||||:||||||
Db          1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||| ||||||||||||||||||||||||.|||| ||  ||| |:|||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||| ||||||||||||||||:|||||:|||| ||||||||||||||||
Db        121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238
              ||||||||||||||:|||||:|||||||||| |||||:|||||    :||:  ||
Db        181 GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELIVVE 240

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
              :|:|||| ||:|||| || || ||||||||||||||||||||||||||||||||||||
Db        241 DEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPD 298

Qy        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358

Qy        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM 418
              ||||||||||||||||||||||||||||||||||||:|||||||||| ||||||||||
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Db        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNM 418

Qy        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPA 478

Qy        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEF 538

Qy        539 SLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDA 598
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db        539 SLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDA 598

Qy        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658

Qy        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||
Db        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 5
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match             92.5%;  Score 3379;  DB 13;  Length 751;
  Best Local Similarity   86.6%;  Pred. No. 3.4e-195;
  Matches  652;  Conservative   19;  Mismatches   22;  Indels   60;  Gaps    4;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||||  |||||| ||||||||||||||||.||||||||||||.||| |||||
Db          1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||:|||||||||||||||||||||||||||||||||||| ||| ||| |:|||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||| ||||||||||||||||||||||||:|||| |||:|||||||||||
Db        121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238
              |||||||||||||||:|||||:|||||||||| |||||:|||||    |:|||: ||
Db        181 GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELIVVE 240

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTISIATTTTTTTESVEEVVR---------- 288
              :|:|||| ||:|||: || || ||||||||||||||||||||'||||||
Db        241 DEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETG 298

Qy        289 ----------------------------------------------VPTTAASTPDAVDK 302
                                                           :|||||||||||||
Db        299 PCRAMISRWYFDVAEGKCAPFFYGGCGGNRNNFDSEEYCMAVCGSVLPTTAASTPDAVDK 358

Qy        303 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 362
              ||||.|||||:|||||||.|||||||||||||||||||||||||||||||||||||||||
Db        359 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 418

Qy        363 KVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKY 422
              |||||||||||||||||||||||||||||||||||||:|||||||||| ||||||||||||
Db        419 KVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKY 478

Qy        423 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEE 482
              ||||||||||||:|||||||||||||||||||||||||||||||||||:||| |||||||||
Db        479 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEE 538

Qy        483 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDD 542
              ||||||||||||||||||||||||||||||||||||||||||||||||:|||||:||||||
Db        539 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEFSLDD 598

Qy        543 LQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEFRH 602
              ||||| || |||||||||:||||:|||||||||||||||||||||:| ||:||| :|||||
Db        599 LQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDAEFRH 658

Qy        603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 662
              |||||||||||'||||||:|||||||||||||||||||||||||||||||||:|||||||
Db        659 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 718

Qy        663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||
Db        719 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751


RESULT 6
Q98SG0
ID   Q98SG0      PRELIMINARY;      PRT;   693 AA.
AC   Q98SG0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein A.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298150; CAC37193.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
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DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   693 AA;  78568 MW;  CAF1DF655C1AB653 CRC64;

  Query Match             87.8%;  Score 3206;  DB 13;  Length 693;
  Best Local Similarity   87.5%;  Pred. No. 7.9e-185;
  Matches  610;  Conservative   37;  Mismatches   44;  Indels    6;  Gaps    4;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||  : ||:|    | || || ||| |||||.||||:|:|||:||||':||::| ||||
Db          1 MLPHITLLVLTV-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               || ||||||||||||||||||||||||||||||||||:|||||||:  |  :||'|'||
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||:||||||||||||||:|||| :||:||||:|||||:|
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFR 179

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVE 238
              ||||||| ||||:: ||||| ||||| |||||| :: | |:|| ||      ||||| ||:
Db        180 GVEFVCCPSAEESESFDSADA-EDDSDAWWGGADADYVDRSDDKAVEAQPDEEEEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
              ||| |||||  |||| ||| |||||||||||||||||||||||||||||||||| ||||||
Db        239 EEETDDDED--DGDEAEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRVPATAASTPD 296

Qy        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358
              ||||||  | |||||  | ||||||| |||::'|:||::||||||||||||:|||||'|||
Db        297 AVDKYLENPNDENEHDRFLKAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQ 356

Qy        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM 418
              ||:||||||:||||||||||||||||||||||||||'||:|||||||||:|| ||:||||||
Db        357 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNM 416

Qy        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478
              ||||||||||||||||||||||||||||||||||||||||||||| |:|||| | || :||
Db        417 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPA 476

Qy        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF 538
              |||:||||||| |||:||||::::||:': |:|:|'||||'|:||:||||| |:| .
Db        477 VAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEF 536

Qy        539 SLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDA 598
              ::::|.||||| |||||.|||||||||||'|||:||||||||:||:|||||| | :|:
Db        537 NIEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDS 596

Qy        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658
              |:|||: ||||||||||||:||||||||||||||||||||:|||:|||:|||||'|:||:|||
Db        597 EYRHDTAYEVHHQKLVFFAEEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHH 656

Qy        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||'||||||:||||||||:||||||||||||
Db        657 GVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 693

RESULT 7
Q98SF9
ID   Q98SF9      PRELIMINARY;      PRT;   695 AA.
AC   Q98SF9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein B.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298151; CAC37194.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   695 AA;  78803 MW;  DC14EB02AFB0204A CRC64;

  Query Match             87.2%;  Score 3182;  DB 13;  Length 695;
  Best Local Similarity   87.0%;  Pred. No. 2.2e-183;
  Matches  607;  Conservative   40;  Mismatches   45;  Indels    6;  Gaps    5;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||  : ||:| |   | ||||| ||| |||||||||||||:||||||||||||::| ||||
Db          1 MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               || |||||||||||||||||||||||||||||||||||:||||||:  | |:|||||||
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||:||||||||||||||:||||  :||:||||||||||||
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR 179

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAEVE 238
              ||||||| ||||:: ||||| |||||||||||| || | |:|| ||     ||||| |||
Db        180 GVEFVCCPTAEESESFDSADA-EDDSDVWWGGADADYVDRSDDKAVEAQPEEEEEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR-VPTTAASTP 297
               |||||| |::|||| ||| ||||||||||||||||||||||||||||| || |: |||
Db        239 EEEADD-DEDDGDETEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRAVPATAVSTP 297

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              |||||||  | |||||  | ||||||| ||||:|||:|||:||||||||||||:|||||||
Db        298 DAVDKYLENPNDENEHDRFLKAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVI 357

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              |||||||||||||||||||||||||||||| ||||:|||||||||||||  |||:||||
Db        358 QHFQEKVESLEQEAANERQQLVETHMARVEATLNDRRRIALENYITALQADPPRPRHVFN 417

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              ||.|||||||||||||||||||||||||||||.|||||||||||||| ||||| |||| ||
Db        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVP 477

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE 537
              |||||:||||| ||||||||:::||:|: |:|||||||||||:||||||||||||||:||
Db        478 AVAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGE 537

Qy        538 FSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLD 597
              |::::||||||||| ||||||||||||||||||||||||||||||||||:|||||| :|
Db        538 FNVEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKREEISEVKMD 597

Qy        598 AEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH 657
              :|:|||: |||||||||||::||||||||||||||||||||||||||||||||||||:||
Db        598 SEYRHDAAYEVHHQKLVFFADEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIH 657

Qy        658 HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||:||||||||||||||||||||
Db        658 HGVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 695

RESULT 8
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Q91963
ID   Q91963      PRELIMINARY;      PRT;   747 AA.
AC   Q91963;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   APP747.
GN   APP747.
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93129227; PubMed=1282805;
RA   Okado H., Okamoto H.;
RT   "A Xenopus homologue of the human beta-amyloid precursor protein:
RT   developmental regulation of its gene expression.";
RL   Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR   EMBL; S52417; AAB24853.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   747 AA;  84893 MW;  A75E81885681D948 CRC64;

  Query Match             84.8%;  Score 3095;  DB 13;  Length 747;
  Best Local Similarity   80.8%;  Pred. No. 4.2e-178;
  Matches  596;  Conservative   36;  Mismatches   42;  Indels   64;  Gaps    5;

Qy         17 ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQE 75
              ||||  ||| |||||||||:|| |||||:|||||:|:::| ||  |: |||||'||||,:
Db         15 ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE 71

Qy         76 VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF 135
              |||||||||||||||||||||||:||||||:  | |:||||||||||||||:|||||,|
Db         72 VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF 131

Qy        136 LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN 195
              |||||||::|||||||||||:|:||||  :|||:||||'||||||:|||||:|| ||.|::
Db        132 LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEESES 191

Qy        196 VDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDEDDEDGDE 253
              |||:| ||| |:|||||| || | ::|| |'   :|||| ||||||  |||||  ||||
Db        192 FDSADAAEDDCDVWWGGADADYVDRSDDKAVEAQPDEEEEVVEVEEEETDDDED--DGDE 249

Qy        254 VEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------------------------- 288
              ||| |||||||||||||||||||||||||||||
Db        250 AEEEPEEPYEEATERTTSIATTITTTTESVEEVVREVCSEQAETGPCRAMISRWYYDVIE 309

Qy        289 ------------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQ 317
                                           :| ,|||||||||||| | ||||' |
Db        310 SKCAQFIYGGCGGNRNNFESDDYCMAVCGSVIPATAASTPDAVDKYLENPNDENEHDRFL 369

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQ 377
              ||||||| ||||:|::||:|:|||||||||||||||||||||'||||:|||'| :|||
Db        370 KAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ 429

Qy        378 LVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 437
              |||||||||||||||||:|||||||||| ||||||||||||||||||:|||||||

Db        430 LVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 489

Qy        438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNY 497
              |||||||||:|||||||||||||||| |||||| |||: |||||:|||||'|| |||||
Db        490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAVAEEIQDEVDELFQKEQNY 549

Qy        498 SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAN 557
              |||:::|||:  |:|||||||||||:|||||||||||:|||:::|||||||'| ||||||
Db        550 SDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPWHSFGVDSVPAN 609

Qy        558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFA 617
              |||||||||||:|||||||||||||||||||||||||||| :|:|:|||: ||||||||||
Db        610 TENEVEPVDARPAADRGLTTRPGSGLINIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669

Qy        618 EDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKM 677
              |:|||||||||||||'|||||||||||||||||||||:|||||||||||||||:||
Db        670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHHGVVEVDAAVIPEERHLTKM 729

Qy        678 QQNGYENPTYKFFEQMQN 695
              ||||||'||||||||||
Db        730 QQNGYENPTYKFFEQMQN 747


RESULT 9
O57394
ID   O57394      PRELIMINARY;      PRT;   699 AA.
AC   O57394;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   EL amyloid precursor protein 699.
GN   EL APP699.
OS   Narke japonica (Electric ray).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Torpediniformes; Narcinoidei; Narkidae; Narke.
OX   NCBI_TaxID=62965;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Electric lobe;
RX   MEDLINE=98129705; PubMed=9461486;
RA   Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA   Suzuki T.;
RT   "cDNA isolation of Alzheimer's amyloid precursor protein from
RT   cholinergic nerve terminals of the electric organ of the electric
RT   ray.";
RL   Biochem. J. 330:29-33(1998).
DR   EMBL; AB005544; BAA24230.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   699 AA;  78879 MW;  952915C309D50E5C CRC64;

  Query Match             81.0%;  Score 2956.5;  DB 13;  Length 699;
  Best Local Similarity   80.5%;  Pred. No. 8.3e-170;
  Matches  567;  Conservative   59;  Mismatches   59;  Indels   19;  Gaps    8;

Qy          2 LPG-LALLLLAAWTA-------RALEVPTDGNAGLL-AEPQIAMFCGRLNMHMNVQNGKW 52
              ||| | :|||||  |        |||||||| |||| ||||||||||:||||:||| |||
Db          5 LPGRLGMLLLAAAAALVLAPLCRALEVPTDGGAGLLAAEPQIAMFCGKLNMHVNVQTGKW 64

Qy         53 DSDPSGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFV 112
              |||||| ||  ||||||:|||||||:|||||||||||:|||||||:|||||| ||| |
Db         65 VSDPSGTNTCDFGTKEGILRYCQEVYPDLQITNVVEANQPITIQNWCKKGRKQCKGHPHIV 124

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
              :|||||||||||||||||||||||:|:|| ||:||:|||||||| :|  |||||||||
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Db        125 VPYRCLVGEFVSDALLVPDKCKFLHREKMDTCESHLYWHTVAKETCSDKIMNLHDYGMLL 184

Qy        173 PCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEE 232
              |||||:|||||||||| |||| :|| | :|:|| |||:| | |||-|   . |    ||
Db        185 PCGIDEFRGVEFVCCPIEEENDKIDS-DMDEEDSDVWWGGDDADYADGG-DKTV----EE 238

Qy        233 EVAEVEEEEADDDEDDEDGDEVEEE-AEEPYEEATERTTSIATTTTTTTESVEEVVRVPT 291
              :  | |||| : | |||| |::::|  |: ||: :| |||   :||:|||::|||'|.||
Db        239 KPIEEEEEEDESDIDDEDDDDLDDEVVEDQYEDPTEHTTS---STTTTTEAIEEVVRVPT 295

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 TAASTPDAVDKYLETPGDENEHAYFQKAKERLEAKHRERMSKIMREWEEAERQAKNLPKA 355

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
              ||||||| ||| |||||||||:||||:|||||| ||||::||||:|||||: |||: |||
Db        356 DKKAVIQRFQEMVESLEQEAASERQQLVETHMARVEAMLNDRRRIALENYIAALQADPPR 415

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
              |||| . |||| |||||||:|||||:||| |||:|||||:||||||| ;: |||| |||
Db        416 PRHVLNALKKYSRAEQKDRQHTLKHFDHVRAVDPEKAAQIKSQVMTHLHVIDERMNQSLS 475

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
              ||| |.:|||||||||||||||:|::| ||:::| :|: '||||:|||:||.:||||.:||
Db        476 LLYKVPSVAEEIQDEVDELLQRERSYMDDMMANSVSDTRISYGNDALVPSLSETKTTIEL 535

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLITRPGSGLTNIKTEEI 591
              || :||| |||||| | |  :|:|||||||||:|||||| ||||:|||| || ||:|||
Db        536 LPDDGEFILDDLQPPHPFVIESIPANTENEVEPVDARPAPDRGLITRPGSGLTGIKTEEI 595

Qy        592 SEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 651
              :|: :: ||: |||||||||||||| :|||||:|||||||||||||:|||.|||||||||
Db        596 AELKMETEFQQDSGYEVHHQKLVFFPKDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 655

Qy        652 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||:|||||:|||||:|||||||||||||||'||||'||||
Db        656 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 699


RESULT 10
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             75.6%;  Score 2759.5;  DB 13;  Length 569;
  Best Local Similarity   93.2%;  Pred. No. 4.6e-158;
  Matches  533;  Conservative   15;  Mismatches   19;  Indels    5;  Gaps    4;

Qy        126 ALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFV 185
              |||||||| |||||||||||||||||||||:|||| |||||||| |||||||||||
Db          1 ALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLSCGIDKFRGVEFV 60

Qy        186 CCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVEEEEAD 243
              |||||||||:|||||:|||||||||| |||||:|||||    |:|||  ||:|:||
Db         61 CCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDFEELIVVEDEDAD 120

Qy        244 DDEDDEDGDEVEEEAEEPYFEATERTTSIATITTTTTTESVEEVVRVPTTAASTPDAVDKY 303
              || ||:|||| || || |||||||||||||||:|||||||||||:|||||||||| |||'
Db        121 DD-DDDDGDEI-EETEEEYEEATERTTSIATITTTTTTESVEEVVRVPTTAASTPDVVDKY 178

Qy        304 LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEK 363
              |||||||||||||||||:|||||||||||||||||'||||'|||||||||||||||||||
Db        179 LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEK 238

Qy        364 VESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYV 423
              |||||||||||||||||||||||||||||:|||||||||| ||||||||||||||||||
Db        239 VESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKYV 298

Qy        424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI 483
              |||||||||||||||||||||||| ||||||||||||||||||| ||||||||||
Db        299 RAEQKDRQHTLKHFEHVRMVDPKKAVQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEEI 358

Qy        484 QDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDL 543
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||| |||||||
Db        359 QDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPTLTETKTTVELLPVVGEFSLDDL 418

Qy        544 QPWHSFGADSVPANTENEVEPVDARPAADRGLITRPGSGLTNIKTEEISEVNLDAEFRHD 603
              |||| || |||||||||||||||||||||||||||||||||:|||:||| :|||||||
Db        419 QPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDAEFRHD 478

Qy        604 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEV 663
              |||||||||||||||||||||||||||||||| ||:|||||||||||||||||||||||
Db        479 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIANVIVITLVMLKKKQYTSIHHGVVEV 538

Qy        664 DAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||| |||||||||||||||||||||||
Db        539 DAAVIP-ERHLSKMQQNGYENPTYKFFEQMQN 569


RESULT 11
Q99K32
ID   Q99K32      PRELIMINARY;      PRT;   607 AA.
AC   Q99K32;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical 68.4 kDa protein (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005490; AAH05490.1; -.
DR   HSSP; P05067; 1AAP.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
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DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
FT   NON_TER       1      1
SQ   SEQUENCE   607 AA;  68391 MW;  BF802214CBA7D172 CRC64;

  Query Match             72.0%;  Score 2627.5;  DB 11;  Length 607;
  Best Local Similarity   85.3%;  Pred. No. 4.4e-150;
  Matches  518;  Conservative    5;  Mismatches    9;  Indels   75;  Gaps    1;

Qy        164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSED 223
              ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||| ||
Db          1 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGED 60

Qy        224 KVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESV 283
              ||||||||||:||||||||||||| ||:||||||||||||||||||:||:||||||||||
Db         61 KVVEVAEEEEVADVEEEEADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESV 120

Qy        284 EEVVR------------------------------------------------------- 288
              ||||
Db        121 EEVVREVCSEQAETGPCRAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGS 180

Qy        289 --------------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHR 328
                                  ::|||:|||||| ||||:||||:||||||||||| |||
Db        181 VSTQSLLKTTSEPLPQDPDKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHR 240

Qy        329 ERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEA 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEA 300

Qy        389 MLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKA 448
              |||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||
Db        301 MLNDRRRLALENYITALQAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKA 360

Qy        449 AQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISE 508
              |||:||||:||||:|||||||||||||||||||||||:||||||||||||||:||||:||
Db        361 AQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISE 420

Qy        509 PRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDAR 568
              :||||||||||||||||||||||||||||||||||:||  |||||||||||||||||:||
Db        421 PRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDAR 480

Qy        569 PAADRGLTTRPGSGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 628
              |||||||||||||||||:||||||||:|:||||:|||:|||:|||||||||||||||||
Db        481 PAADRGLTTRPGSGLTNIKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAII 540

Qy        629 GLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYK 688
              :||||||:|||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        541 GLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYK 600

Qy        689 FFEQMQN 695
              ||||||:
Db        601 FFEQMQN 607

RESULT 12
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             71.4%;  Score 2605;  DB 13;  Length 534;
  Best Local Similarity   94.4%;  Pred. No. 8.3e-149;
  Matches  504;  Conservative   14;  Mismatches   12;  Indels    4;  Gaps    3;

Qy        164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSED 223
              ||||||:|||||||||||||||||||||||||:||||||||:||||||||||| ||||||:|
Db          3 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDD 62

Qy        224 KVVE--VAEEEEVAEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTE 281
              |:||    |:||:  ||:|:|||:||||:||  ||:|||||||||||||||||||||||
Db         63 KVVEEQPEEDEELTVVEDEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTE 120

Qy        282 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 180

Qy        342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENY 401
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        181 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENY 240

Qy        402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ITALQTVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 300

Qy        462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 521
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IYERMNQSLSFLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 360

Qy        522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGS 581
              ||||||||||||:|||||||||||| || ||||||||||||||||||||||||||||||||
Db        361 LTETKTTVELLPVDGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGS 420

Qy        582 GLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 641
              ||||:||||:||| :|||||||||||||||||||||||||||||||||||||||||||||
Db        421 GLTNVKTEEVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 480

Qy        642 VITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 534

RESULT 13
O73683
ID   O73683      PRELIMINARY;      PRT;   780 AA.
AC   O73683;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Tetraodon fluviatilis (Puffer fish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC       WITH Xil-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC       RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC       NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC       PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
CC       BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    780       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                HOMOLOG.
FT   CHAIN       682    724       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    732       POTENTIAL.
FT   DOMAIN      733    780       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      323    382       BPTI/KUNITZ INHIBITOR.
FT   SITE        769    772       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    327    378       BY SIMILARITY.
FT   DISULFID    336    361       BY SIMILARITY.
FT   CARBOHYD    560    560       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   780 AA;  88238 MW;  60071BE94520191D CRC64;

  Query Match           70.3%;  Score 2568;  DB 13;  Length 780;
  Best Local Similarity 65.3%;  Pred. No. 2.3e-146;
  Matches  512;  Conservative   71;  Mismatches   95;  Indels  106;  Gaps   10;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
              |||:|  :  : |||| : ||||.||:|:|:|.|:::|.:|||:|||: . |||||.| ||
Db          8 LLLVAAASTLAAEVPTDVSMGLLAEPQVAMFCGKINMHINVQSGKWEPDPSGTKSCIGTK 67

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
              |||||||||||||||||||||:||||||:||||.:: | :|:|||:|||:|:|||
Db         68 EGILQYCQEVYPELQITNVVEANQPVSIQNWCKKGRKQCRSHMHIVVPYRCLVGEFVSDA 127

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
              |||||||||||||||: ||:|||||||||||:| ::: |||||:|||||:.:|| :|||
Db        128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVEFVC 187

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS----------EDKVVEVAEEE 232
              || ||   ::|| : : ||||||||||| ||:| |                ||| ||
Db        188 CP-AEAERDMDSTEKDADDSDVWWGGADNDYSDNSMVREPEPAEQQEETRPSVVEEEEEG 246

Qy        233 EVAEVEEEE----------------ADDDEDDEDGDEVEEEAEEPYEEATERTISIA 273
              |:|: ::||                |||:|:::| ||::   |    :| | ||::|
Db        247 EVAQEDDEEEEEVLDTDQDGDEEDHEAADDEEEEDVDEIDAFGESDDVDADEPTTNVA 306

Qy        274 ---TTITTTTESVEEVVR---------------------------------------- 288
                 |||||||||||||
Db        307 MTTTTITTTTESVEEVVRMFCWAHADTGPCTASMPSWYFDAVDGRTMYELMYGGCGGNMN 366

Qy        289 --------------VPTIAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQ 333
                           |||   |:|||| |||| |||||||||||| ||||||||||
Db        367 NFESEEYCLSVCSSVVPTDMPSSPDAVDHYLETPADENEHAHFQKAKESLEAKHRERMSQ 426

Qy        334 VMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDR 393
              |||||| |||||||:|||| ||| |||||:|||||:|||||:|||||||||:|||
Db        427 VMREWEEAERQAKNLPRADKKIVIQRFQEKVEALEQEAASERQQLVETHMARVEAILNDR 486

Qy        394 RRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRS 453
              |||||||:|||| ||||||||::|||||||||||||||||||||||||||||||||||
Db        487 RRLALENYLTALQQDPPRPRHVFSLLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRP 546

Qy        454 QVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
              ||:|||||| ||||||| ||| || ||::|||:| ||||:||      |||: :: |:||
Db        547 QVLTHLRVIEERMNQSLGLLYKVPGVADDIQDQV-ELLQREQAEMAQQLANLQTDVRVSY 605

Qy        514 GNDALMPSLTETKITVELLPVNGEFSLDDLQPWH--SFGADSVPANTENEVEPVDARPAA 571
              |||||||          :||| | :| :  |  || |||||||||||||||||||||||
Db        606 GNDALMPDQELGDGQADLLP--QEDTLGGVGFVHPESFN----QLNTENQVEPVDSRPTF 659

Qy        572 DRGLTTRPGSGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLM 631
              :|||: |||   :|    | : |: :: | |  : |||||||||||||||||||||||||
Db        660 ERGVPTRP---VIGKSMEAVPELRMETEDRQSTEYEVHHQKLVFFAEDVGSNKGAIIGLM 716

Qy        632 VGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
              |||||||||||||||||:|||||||||::|||||||||||||||||||||||||||||||
Db        717 VGGVVIATVIVITLVMLRKKQYTSIHHGIIEVDAAVTPEERHLSKMQQNGYENPTYKFFE 776

Qy        692 QMQN 695
              |:||
Db        777 QMQN 780
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RESULT 14
Q90W28
ID   Q90W28      PRELIMINARY;      PRT;   738 AA.
AC   Q90W28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid precursor protein.
GN   APPA OR APP.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Expression analysis of zebrafish app.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389401; AAK64495.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
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DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   738 AA;  83577 MW;  AF480F6D308FD298 CRC64;

  Query Match             69.1%;  Score 2524;  DB 13;  Length 738;
  Best Local Similarity   66.3%;  Pred. No. 9.5e-144;
  Matches  500;  Conservative   79;  Mismatches   91;  Indels   84;  Gaps   14;

Qy          5 LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCID 64
Db          6 LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPDPSGSKSCIG 65

Qy         65 TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVS 124
Db         66 NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS 125

Qy        125 DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF 184
Db        126 DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF 185

Qy        185 VCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADD 244
Db        186 VCCP-ADAGKESESAAVEEDDSDVWWGGAEADYTENSMTR--DAAAEPAVLE-DDEDADE 241

Qy        245 DED-DEDGD-----EVEEEAEEPYEEATERTT-SIATTTTTTTESVEEVVR--------- 288
Db        242 EEDEDQDGDGDRDEKIEEEEEE--EERTQSTSAALTSTTTTTTESVEEVVREVCFASAET 299

Qy        289 ----------------------------------------------VPTTAASTPDAVD 301
Db        300 GPCRAMLSRWYYVREERRCAPFIYGGCGGNRNNFESEEYCLSVCSGVLPTPSSSPPDAVD 359

Qy        302 KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQ 361
Db        360 RYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAKSLPRNDKKAVIQHFQ 419

Qy        362 EKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKK 421
Db        420 EKVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQADPPRPRHVFSLLKK 479

Qy        422 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAE 481
Db        480 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVAD 539

Qy        482 EIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLD 541
Db        540 DIQDQV-ELLQREQGEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTGGFG 595

Qy        542 DLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEFR 601
Db        596 FIHP-ESFN----QPNTHNQVEPVDARPVPDLDLATRPVSGL---KPDDIPELRMEAEER 647

Qy        602 HDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVV 661
Db        648 HS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIVITLVMLRKKQYTSIHHGII 704

Qy        662 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db        705 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 738

RESULT 15
Q8UUR9
ID   Q8UUR9      PRELIMINARY;      PRT;   694 AA.
AC   Q8UUR9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Putative membrane protein.
GN   APPB.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11862463;
RA   Musa A., Lehrach H., Russo V.E.A.;
RT   "Distinct expression patterns of two zebrafish homologues of the human
RT   APP gene during embryonic development.";
RL   Dev. Genes Evol. 211:563-567(2001).
DR   EMBL; AJ315639; CAC85736.1; -.
DR   ZFIN; ZDB-GENE-020220-1; appb.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   694 AA;  79228 MW;  2B03382D411162DC CRC64;

  Query Match             68.1%;  Score 2487.5;  DB 13;  Length 694;
  Best Local Similarity   68.0%;  Pred. No. 1.4e-141;
  Matches  478;  Conservative   96;  Mismatches   98;  Indels   31;  Gaps    9;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
Db          9 LLLMLITLSLAIEVPSDDSVGLLAEPQVAMFCGKLNMHINVQSGKWEPDPTGTKSCISTK 68

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
Db         69 EGILKYCQEVYPDLQITNVVEANQPVSIQNWCKMGRRQCRSHTHIVVPYRCLVGEFVSDA 128

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
Db        129 LLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVC 188

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS--EDKVV-----EVAEEEEVAEVEE 239
Db        189 CPMEEQKD-LDSEEQEEANSDVWWGGAETEYTDASVLKEQVTAKPDPAVTEDDEDLNNEE 247

Qy        240 EEADDDEDDEDGDEVEEEAEE-----PYEEATERTTSIA--TTTTTTTESVEEVVRVPTT 292
Db        248 EEVWDNDEDGDGEDDEDEEDDDEDIIDEQDTSEQTSNIAMTTTTTTTESIEEVVRVPTM 307

Qy        293 AASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKAD 352
Db        308 APSPADAVDRYLEAPGDMNEHMRFQKAKESLEAKHREKMSEVMREWEEAERQAKNLPRAD 367

Qy        353 KKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRP 412
Db        368 KKTIIQRFQEKVESLEKEAAGERQQLVETHMARVEALLNDRRRQALESYLSSLQSDQPRP 427

Qy        413 RHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSL 472
Db        428 RQVLNLLKKYIRAEQKDRQHTLKHFEHVREVDPKKASQIRPFVMTHLRVIEERMNQSLGY 487

Qy        473 LYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELL 532
Db        488 LYKVPQVANDIQDQVAVLVQRDQAEVTQQLSSLQSKMRVSYGNDALMPDLPDSTTPLDNL 547

Qy        533 PVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEIS 592
Db        548 PPEQD-GLGFIHP-ESFN----QANTDNHVEPVDARPIPERGLPTRP---------EIP 591

Qy        593 EVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQ 652
Db        592 KVRLDIEERHNAGYDVRDKRLMFLAEDMGSNKGAIIGLMVGGVVIATVIVITLVMLRKKQ 651
```

```
Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||.|||:|:|.||||||||||:|||||||..:|||.|:|||
Db        652 YTSIHHGVIEVDAAVTPEERHLAKMQQNGYENPTYKFFEQMQN 694

Search completed: October 2, 2003, 14:02:38
Job time : 42 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:09 ; Search time 38.3333 Seconds
(without alignments)
2886.063 Million cell updates/sec

Title: US-09-806-194-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3653	100.0	697	21	AAY88430	Human APP695-VF-KK
2	3653	100.0	697	22	AAE10637	Human amyloid prot
3	3653	100.0	697	22	AAE06867	Human amyloid prec
4	3653	100.0	697	22	AAU06611	Human Amyloid prec
5	3653	100.0	697	22	AAU07210	Human beta-amyloid
6	3653	100.0	697	22	AAE02589	Human amyloid prec
7	3653	100.0	697	23	ABB78598	Human APP695-VF-KK
8	3646	99.8	697	21	AAY88428	Human APP696-KK am
9	3646	99.8	697	22	AAE10635	Human amyloid prot
10	3646	99.8	697	22	AAE06865	Human amyloid prec
11	3646	99.8	697	22	AAU06609	Human Amyloid prec
12	3646	99.8	697	22	AAU07208	Human beta-amyloid
13	3646	99.8	697	22	AAE02587	Human amyloid prec
14	3646	99.8	697	23	ABB78596	Human APP695-KK pr
15	3643	99.7	695	18	AAW19498	APP695 mutant A-be
16	3643	99.7	695	18	AAW19484	APP695 mutant A-be
17	3643	99.7	695	21	AAY88436	Human APP695-VF am
18	3643	99.7	695	22	AAE10634	Human amyloid prot
19	3643	99.7	695	22	AAE06864	Human amyloid prec
20	3643	99.7	695	22	AAU06608	Human Amyloid prec
21	3643	99.7	695	22	AAU07207	Human beta-amyloid
22	3643	99.7	695	22	AAE02586	Human amyloid prec
23	3643	99.7	695	23	ABB78595	Human APP695-VF pr
24	3638	99.6	697	21	AAY88429	Human APPSW-KK ami
25	3638	99.6	697	22	AAE10636	Human amyloid prot
26	3638	99.6	697	22	AAE06866	Human amyloid prec
27	3638	99.6	697	22	AAU06610	Human Amyloid prec
28	3638	99.6	697	22	AAU07209	Human beta-amyloid
29	3638	99.6	697	22	AAE02588	Human amyloid prec
30	3638	99.6	697	23	ABB78597	Human APP695-Sw-KK
31	3636	99.5	695	9	AAP81692	Sequence of human
32	3636	99.5	695	13	AAR26338	APP695. Homo sapi
33	3636	99.5	695	18	AAW19481	APP695 mutant A-be
34	3636	99.5	695	19	AAY20233	Human beta-amyloid
35	3636	99.5	695	20	AAY07221	Amyloid precursor
36	3636	99.5	695	21	AAY88434	Human APP695 amino
37	3636	99.5	695	21	AAY44705	Human beta amyloid
38	3636	99.5	695	22	AAE10632	Human wild-type am
39	3636	99.5	695	22	AAE06862	Human wild-type am
40	3636	99.5	695	22	AAU06606	Human Amyloid prec
41	3636	99.5	695	22	AAE02584	Human amyloid prec
42	3636	99.5	695	23	ABG32721	Human amyloid prec
43	3636	99.5	695	23	ABB78593	Human APP695 prote
44	3636	99.5	695	23	AAG68315	Human amyloid prec
45	3636	99.5	695	24	ABB99604	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAY88430
ID AAY88430 standard; Protein; 697 AA.
XX
AC AAY88430;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human APP695-VF-KK amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APP695-VF-KK.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15667.
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

PT the beta secretase site to produce amyloid beta peptide -
XX
PS Claim 133; Page 148-153; 188pp; English.
XX
CC This sequence represents a modified version of the human amyloid
CC precursor protein (APP) amino acid sequence. The sequence is used in an
CC example of the method of the invention, to show that modification of APP
CC increases beta amyloid protein processing. The invention relates to a
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC amyloid precursor protein (APP). The protease contains a sequence
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC separated by 100-300 amino acids. When mutated the APP gene causes an
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC nucleotide sequence, and a cell line comprising the vector. Methods for
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease.
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3653; DB 21; Length 697;
Best Local Similarity 100.0%; Pred. No. 8.3e-257;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGIK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||'||||,|||||||||||||| |||||| |||||' ||||||||||, |||||,
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |:|||||||:|||||:|||||'||||||'|||||.|||||, ||||,,|||' ||||',|
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              |||||||||||||'|||||,|||||||||||||||||||||' |||'||||,'||||'|||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
```

```
Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

RESULT 2
AAE10637
ID AAE10637 standard; Protein; 697 AA.
XX
AC AAE10637;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.
XX
KW Human; aspartyl protease 1; Aspl; amyloid precursor protein;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW APP695-VF-KK; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 642
FT /note= "Wild-type Val substituted with Phe"
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowksi MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR N-PSDB; AAD17873.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
PS Example 8; Page 120-122; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC Aspl proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Aspl alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Aspl alpha-secretase activity, where modulators that increase
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Aspl proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-VF-KK (APP695-VF-KK) isoform. This sequence
CC is obtained by the addition of two lysine residues (KK motif) at
CC the C-terminus of App695-VF isoform which is generated by the London
CC mutation in APP695, where Val at position 642 is replaced with Phe.
CC APP695-VF-KK isoform is useful for assaying the beta-secretase
CC activity of human aspartyl protease 2a (hu-Asp2a) protein.

```
XX
SQ   Sequence   697 AA;

  Query Match           100.0%;  Score 3653;  DB 22;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-257;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 3
AAE06867
ID   AAE06867 standard; Protein; 697 AA.
XX
AC   AAE06867;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.
XX
KW   Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-VF-KK;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; gene therapy; APP695-VF-KK; mutant;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild type Val substituted with Phe"
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00799.
XX
PR   09-MAY-2001; 2001WO-IB00799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-483072/52.
DR   N-PSDB; AAD13029.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 8; Page 150-152; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting
CC   Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC   blots. The present sequence is modified human amyloid precursor
CC   protein 695-VF-KK (APP695-VF-KK) isoform. APP695-VF-KK isoform is
CC   obtained by addition of two Lys residues (KK motif) at the C-terminal
CC   end of APP695-VF isoform. APP695-VF isoform is obtained by London V-F
CC   mutation in APP695 isoform, where Val at position 642 is replaced with
CC   Phe. APP695-VF-KK isoform is useful for assaying the beta-secretase
CC   activity of human aspartyl protease 2a (Hu-Asp2a) protein.
XX
SQ   Sequence   697 AA;

  Query Match           100.0%;  Score 3653;  DB 22;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-257;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
```

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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLITRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLITRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 4
AAU06611
ID   AAU06611 standard; Protein; 697 AA.
XX
AC   AAU06611;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-VF-KK.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-VF-KK; London mutant; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val substituted by Phe"
FT   Misc-difference 696..697
FT                   /note= "2 Extra Lys residues added compared to
FT                   wild-type APP695"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00798.
XX
PR   09-MAY-2001; 2001WO-IB00798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-502549/55.
DR   N-PSDB; AAS11525.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 8; Page 150-152; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp
CC   proteins and vectors expressing them, and a polypeptide (isoform of
CC   amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC   APP or its fragment containing an APP cleavage site recognizable by a
CC   mammalian beta-secretase, and further comprising two lysine residues at
CC   the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC   APP fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and
CC   amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease.
CC   APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC   is associated with increased levels of Abeta processing is useful in
CC   assays relating the Alzheimer's research. The expression vector is useful
CC   for recombinantly expressing APP. Nucleic acids that hybridise to
CC   Asp oligonucleotides are useful as probes or primers. The probes are
CC   useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence is the human
CC   APP695 mutant, APP695-VF-KK which has 2 extra Lys residues added at the
CC   C-terminus compared to APP695-VF (the London mutation). The mutation
CC   alters the specificity of the APP gamma-secretase activity and increases
CC   the rate of processing of the amyloid Abeta peptide.
XX
SQ   Sequence   697 AA;
```

```
  Query Match             100.0%;  Score 3653;  DB 22;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-257;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 5
AAU07210
ID   AAU07210 standard; Protein; 697 AA.
XX
AC   AAU07210;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human beta-amyloid protein precursor, APP695-VF-KK.
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; APP695-VF-KK.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild type Val substituted by Phe"
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00797.
XX
PR   09-MAY-2001; 2001WO-IB00797.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-502548/55.
DR   N-PSDB; AAS11710.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 8; Page 150-152; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing
CC   an APP cleavage site recognisable by a mammalian beta-secretase, and
CC   further comprising two lysine residues at the carboxyl terminus of the
CC   amino acid sequence of the mammalian APP or APP fragment. The
CC   polypeptides are used for assaying for modulators of beta-secretase
CC   activity; identifying agents that inhibit the APP processing activity
CC   of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC   modulate the activity of Asp2; and for reducing cellular production of
CC   amyloid beta (Abeta) from APP. Agents identified by the above methods
CC   are useful for treating Alzheimer's disease; and for identifying
CC   modulators of amyloid-beta (Abeta) peptide production, for use in
CC   designing therapeutics for the treatment or prevention of Alzheimer's
CC   disease. Probes and primers derived from Asp nucleic acid sequences
CC   are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence represents the
CC   amino acid sequence of human amyloid protein precursor, APP695-VF-KK,
CC   used in the method of the invention.
XX
SQ   Sequence   697 AA;

  Query Match             100.0%;  Score 3653;  DB 22;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-257;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 6
AAE02589
ID   AAE02589 standard; Protein; 697 AA.
XX
AC   AAE02589;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).
XX
KW   Human; alpha-secretase; therapy; amyloid precursor protein 695-VF-KK;
KW   APP695-VF-KK; Alzheimer's disease; antialzheimer's.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26080.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M, Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   N-PSDB; AAD06747.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Example 8; Page 149-151; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human APP695-VF-KK. This
CC   sequence is characterised by a V to F alteration at position 642
CC   and contains two carboxy-terminal lysine residues.
XX
SQ   Sequence   697 AA;

  Query Match           100.0%;  Score 3653;  DB 22;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-257;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 7
ABB78598
ID   ABB78598 standard; Protein; 697 AA.
XX
AC   ABB78598;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human APP695-VF-KK protein sequence SEQ ID NO:20.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW   proteolytic; amyloid precursor protein; APP.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-0025934.
XX
PR   23-SEP-1999;   99US-155493P.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-169232P.
PR   22-SEP-2000; 2000GB-0023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ, Gurney M;
XX
DR   WPI; 2002-396337/43.
DR   N-PSDB; ABL52465.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect
PT   aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT   disease -
XX
PS   Example 8; Page 120-122; 182pp; English.
XX
CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
```

CC substrate (I) which comprises a peptide of no more than 50 amino acids, CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu- CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with CC (I) under acidic conditions; and (b) determining the level of hu-Asp1 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a CC nucleotide sequence that hybridises under stringent conditions to the CC non-coding strand complementary to a defined 1894 nucleotide sequence CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane CC domain); (3) a purified polynucleotide (III') comprising a sequence that CC hybridises under stringent conditions to (III) (the nucleotide sequence CC encodes a polypeptide further lacking a pro-peptide domain corresponding CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV) CC comprising (III) or (III'); and (5) a host cell (V) transformed or CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease CC substrate (I) may be used as an enzyme substrate in assays to detect CC aspartyl protease activity, (II) and therefore diagnose diseases CC associated with aberrant hu-Asp1 expression and activity such as CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present CC sequence represents human amyloid precursor protein APP695-VF-KK, which CC is given in an example from the present invention.
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3653; DB 23; Length 697;
Best Local Similarity 100.0%; Pred. No. 8.3e-257;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
```

```
Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

RESULT 8
AAY88428
ID AAY88428 standard; Protein; 697 AA.
XX
AC AAY88428;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human APP696-KK amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APP696-KK.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15665.
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at
PT the beta secretase site to produce amyloid beta peptide -
XX
PS Claim 132; Page 137-141; 183pp; English.
XX
CC This sequence represents a modified version of the human amyloid
CC precursor protein (APP) amino acid sequence. The sequence is used in an
CC example of the method of the invention, to show that modification of APP
CC increases beta amyloid protein processing. The invention relates to a
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC amyloid precursor protein (APP). The protease contains a sequence
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC separated by 100-300 amino acids. When mutated the APP gene causes an
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC nucleotide sequence, and a cell line comprising the vector. Methods for
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease.
XX
SQ Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 21; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.7e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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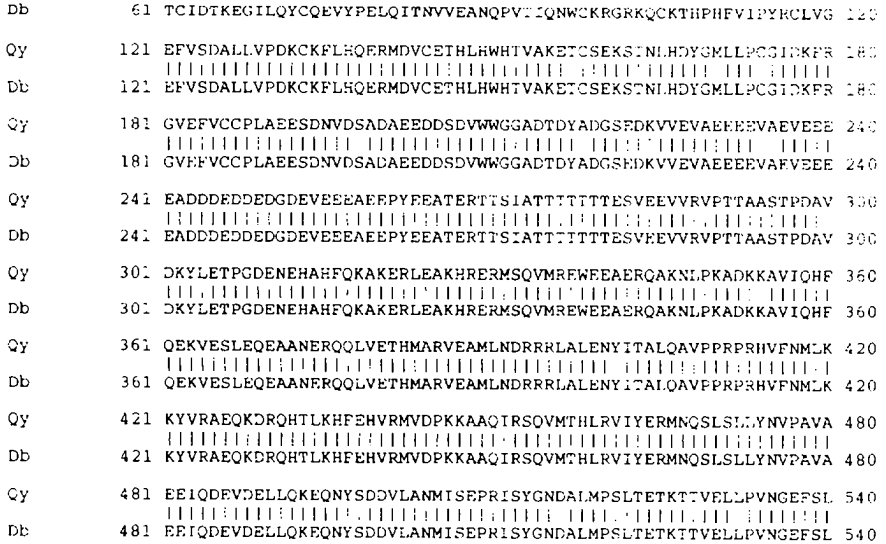
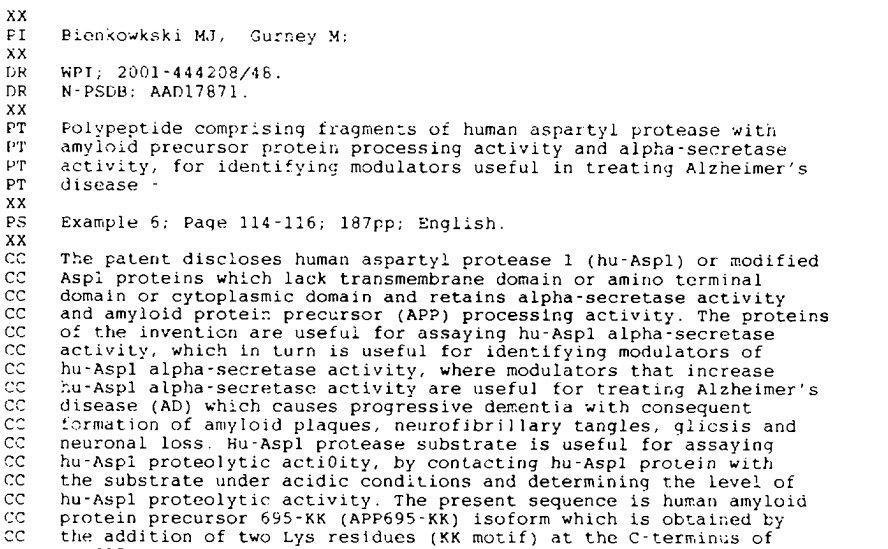


RESULT 9
AAE10635
ID AAE10635 standard; Protein; 697 AA.
XX
AC AAE10635;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human amyloid protein precursor 695-KK (APP695-KK) isoform.
XX
KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-KK;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.



XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR N-PSDB; AAD17871.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
PS Example 6; Page 114-116; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC Aspl proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Aspl alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Aspl alpha-secretase activity, where modulators that increase
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Aspl proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-KK (APP695-KK) isoform which is obtained by
CC the addition of two Lys residues (KK motif) at the C-terminus of
CC APP695 protein.
XX
SQ Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 22; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.7e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||||||| ||||||||||||||||||| |||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 10
AAE06865
ID   AAE06865 standard; Protein; 697 AA.
XX
AC   AAE06865;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-KK (APP695-KK) isoform.
XX
KW   Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
KW   beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW   neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW   neuroprotective; antisense therapy; gene therapy; APP695-KK; mutant;
KW   mutein.
XX
OS   Homo sapiens.
XX
PN   WO200150829-A2.
XX
PD   19-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00799.
XX
PR   09-MAY-2001; 2001WO-IB00799.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-483072/52.
DR   N-PSDB; AAD13027.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC   precursor protein (APP) isoforms and their corresponding DNA molecules.
CC   Human aspartyl proteases can act as beta-secretase proteases useful for
CC   treating Alzheimer's disease. APP isoforms are useful for identifying
CC   modulators of amyloid-beta peptide production, for use in designing
CC   therapeutics for the treatment and prevention of Alzheimer's disease,
CC   dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC   and neuronal loss. APP isoforms are also used in methods for identifying
CC   inhibitors and modulators of human Asp2 activity. The invention relates
CC   to a method for identifying agents that modulate the activity of human
CC   aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC   as a means to screen in cellular assays for the inhibitors of beta- and
CC   gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC   polymerase chain reactions (PCR). The probes are useful for detecting
CC   Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC   blots. The present sequence is modified human amyloid precursor
CC   protein 695-KK (APP695-KK) isoform. APP695-KK isoform is obtained by
CC   addition of two Lys residues (KK motif) at the C-terminal end of APP695
CC   isoform.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3646;  DB 22;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHIVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATITTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATITTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              ||||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 11
AAU06609
ID   AAU06609 standard; Protein; 697 AA.
XX
AC   AAU06609;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-KK.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-KK; mutant; mutein.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 696..697
FT                   /note= "2 Extra Lys residues added compared to
FT                   wild-type APP695"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00798.
XX
PR   09-MAY-2001; 2001WO-IB00798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-502549/55.
DR   N-PSDB; AAS11523.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp
CC   proteins and vectors expressing them, and a polypeptide (isoform of
CC   amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC   APP or its fragment containing an APP cleavage site recognizable by a
CC   mammalian beta-secretase, and further comprising two lysine residues at
CC   the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC   APP fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and
CC   amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease.
CC   APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC   is associated with increased levels of Abeta processing is useful in
CC   assays relating the Alzheimer's research. The expression vector is useful
CC   for recombinantly expressing APP. Nucleic acids that hybridise to
CC   Asp oligonucleotides are useful as probes or primers. The probes are
CC   useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence is the human
CC   APP695 mutant, APP695-KK which has 2 extra Lys residues added at
CC   the C-terminus compared to the wild-type APP695. The mutation alters the
CC   specificity of the APP gamma-secretase activity and increases the rate
CC   of processing of the amyloid Abeta peptide.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3646;  DB 22;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 12
AAU07206
ID   AAU07208 standard; Protein; 697 AA.
XX
AC   AAU07208;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human beta-amyloid protein precursor, APP695-KK.
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; APP695-KK.
XX
OS   Homo sapiens.
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00797.
XX
PR   09-MAY-2001; 2001WO-IB00797.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
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PI   Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR   WPI; 2001-502548/55.
DR   N-PSDB; AAS11708.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity -
XX
PS   Example 6; Page 144-146; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing
CC   an APP cleavage site recognisable by a mammalian beta-secretase, and
CC   further comprising two lysine residues at the carboxyl terminus of the
CC   amino acid sequence of the mammalian APP or APP fragment. The
CC   polypeptides are used for assaying for modulators of beta-secretase
CC   activity; identifying agents that inhibit the APP processing activity
CC   of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC   modulate the activity of Asp2; and for reducing cellular production of
CC   amyloid beta (Abeta) from APP. Agents identified by the above methods
CC   are useful for treating Alzheimer's disease; and for identifying
CC   modulators of amyloid-beta (Abeta) peptide production, for use in
CC   designing therapeutics for the treatment or prevention of Alzheimer's
CC   disease. Probes and primers derived from Asp nucleic acid sequences
CC   are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC   Northern and Southern blots. The present sequence represents the
CC   amino acid sequence of human amyloid protein precursor, APP695-KK,
CC   used in the method of the invention.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3646;  DB 22;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||.|||||||||||||||||||||||||||||||||||||||||| |||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              |||||||||||:|||||||||||||||||||||||||||| |||| |||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPIYKFFEQMQNKK 697
              ;|||||.|||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPIYKFFEQMQNKK 697


RESULT 13
AAE02587
ID   AAE02587 standard; Protein; 697 AA.
XX
AC   AAE02587;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein 695-KK (APP695-KK).
XX
KW   Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
KW   therapy; Alzheimer's disease; antialzheimer's.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26080.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M, Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   N-PSDB; AAD06745.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Example 6; Page 143-145; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human APP695-KK. This
CC   sequence contains two carboxy-terminal lysine residues.
XX
SQ   Sequence   697 AA;

  Query Match             99.8%;  Score 3646;  DB 22;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
```

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Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               ||||||||:|||||||||||||||||||||||||||| |||||||||||||||| |||.
Db          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
               ||||||||||||||||||||||||||||||||||||
Db         661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

```
RESULT 14
ABB78596
ID   ABB78596 standard; Protein; 697 AA.
XX
AC   ABB78596;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human APP695-KK protein sequence SEQ ID NO:16.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW   proteolytic; amyloid precursor protein; APP.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-0025934.
XX
PR   23-SEP-1999;   99US-155493P.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-169232P.
PR   22-SEP-2000; 2000GB-0023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowski MJ, Gurney M;
XX
DR   WPI; 2002-396337/43.
DR   N-PSDB; ABL52463.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect
PT   aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT   disease -
XX
PS   Example 6; Page 114-116; 182pp; English.
XX
CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC   proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the
CC   non-coding strand complementary to a defined 1804 nucleotide sequence
CC   (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC   Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC   domain); (3) a purified polynucleotide (III') comprising a sequence that
CC   hybridises under stringent conditions to (III) (the nucleotide sequence
CC   encodes a polypeptide further lacking a pro-peptide domain corresponding
CC   to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC   comprising (III) or (III'); and (5) a host cell (V) transformed or
CC   transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC   substrate (I) may be used as an enzyme substrate in assays to detect
CC   aspartyl protease activity, (II) and therefore diagnose diseases
CC   associated with aberrant hu-Asp1 expression and activity such as
CC   Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC   hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC   sequence represents human amyloid precursor protein APP695-KK, which is
CC   given in an example from the present invention.
XX
SQ   Sequence   697 AA;
```

```
  Query Match           99.8%;  Score 3646;  DB 23;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-256;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
               ||||||||:|||||||||||||||||||||||||||||||||||||:|||||||||||||
Db           1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVAEVEEE 240
               ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              |||.|||||||||||||||||||||||||||||||||.|| |||||||||| |||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              |||||||||||||||||.|||||||||||| |||||||||| ||||| |||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              |||||||||||||||||||||||||||||||||.||||| ||| |||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 15
AAW19498
ID   AAW19498 standard; protein; 695 AA.
XX
AC   AAW19498;
XX
DT   08-SEP-1997  (first entry)
XX
DE   APP695 mutant A-beta-containing protein.
XX
KW   Alzheimer's disease; transgenic mammal; beta-amyloid precursor protein;
KW   APP.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val is preferably substituted by Phe"
XX
PN   WO9640896-A1.
XX
PD   19-DEC-1996.
XX
PF   07-JUN-1996;   96WO-US09857.
XX
PR   07-JUN-1995;   95US-0480653.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Games KD,  McConlogue LC,  Rydel RE,  Schenk DB,  Seubert PA;
XX
DR   WPI; 1997-052309/05.
XX
PT   Testing compounds for an effect on an Alzheimer's disease marker -
PT   uses non-human transgenic animals which can control expression of
PT   major forms of beta-amyloid precursor protein
XX
PS   Claim 23; Page -; 139pp; English.
XX
CC   A novel method has been produced for testing compounds for an effect on
CC   an Alzheimer's disease (AD) marker. The method involves: administering
CC   the compound to be tested to a non-human transgenic mammal, or mammalian
CC   cells derived from the transgenic mammal, where the transgenic mammal
CC   has a nucleic acid construct stably incorporated into the genome which
CC   comprises a promoter for expression of the construct in a mammalian cell
CC   operably linked to a region encoding an A-beta-containing protein. The
CC   region is selected from DNA encoding the A-beta-containing protein
CC   consisting of all, or a contiguous portion of APP770, APP751 or APP695,
CC   or a mutant comprising a mutation in one or more of amino acids 669,
CC   670, 671, 690, 692 and 717, which includes amino acids 672-714 of human
CC   beta-amyloid precursor protein (APP). The present sequence represents a
CC   mutant APP695 protein in which the codon encoding amino acid 717 is
CC   mutated (see features table). The amino acid positions referred to in
CC   the specification are as they appear in APP770 (see AAW19497) i.e.
CC   position 717 represents position 642 in APP695, and 698 in APP751. The
CC   larger forms of APP (APP751, APP770) consist of APP695 plus one or two
CC   additional domains. The method also involves detecting or measuring the
CC   AD marker such that any difference between the marker in the transgenic
CC   animal, or mammalian cells derived from the transgenic mammal, to which
CC   the compound has not been administered, is observed, where an observed
CC   difference in the marker indicates that the compound has an effect on
CC   the marker. The transgenic animals, or cells are used to screen for
CC   compounds which alter the pathological course of AD as measured by their
CC   effect on the amount and/or histopathology of AD markers in animals as
CC   well as behavioural alterations.
CC   N.B. The present sequence is shown in the specification, but has
CC   been derived from SEQ ID NO:2 which is on pages 103-105.
XX
SQ   Sequence   695 AA;
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```
  Query Match           99.7%;  Score 3643;  DB 18;  Length 695;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-256;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTISIATITTTTTESVEEVVRVPITAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATITTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              |||||.|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Job time : 40.3333 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:59 ; Search time 18 Seconds
(without alignments)
1638.370 Million cell updates/sec

Title: US-09-806-194-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3653	100.0	697	4	US-09-548-372D-20	Sequence 20, Appl
2	3653	100.0	697	4	US-09-548-367D-20	Sequence 20, Appl
3	3653	100.0	697	4	US-09-551-853D-20	Sequence 20, Appl
4	3646	99.8	697	4	US-09-548-372D-16	Sequence 16, Appl
5	3646	99.8	697	4	US-09-548-367D-16	Sequence 16, Appl
6	3646	99.8	697	4	US-09-551-853D-16	Sequence 16, Appl
7	3643	99.7	695	4	US-09-548-372D-14	Sequence 14, Appl
8	3643	99.7	695	4	US-09-548-367D-14	Sequence 14, Appl
9	3643	99.7	695	4	US-09-551-853D-14	Sequence 14, Appl
10	3638	99.6	697	4	US-09-548-372D-18	Sequence 18, Appl
11	3638	99.6	697	4	US-09-548-367D-18	Sequence 18, Appl
12	3638	99.6	697	4	US-09-551-853D-18	Sequence 18, Appl
13	3636	99.5	695	1	US-08-123-702-2	Sequence 2, Appli
14	3636	99.5	695	2	US-08-104-165-1	Sequence 1, Appli
15	3636	99.5	695	3	US-08-464-250-1	Sequence 1, Appli
16	3636	99.5	695	4	US-08-464-250-1	Sequence 1, Appli
17	3636	99.5	695	4	US-09-458-481B-7	Sequence 7, Appli
18	3636	99.5	695	4	US-09-458-481B-8	Sequence 8, Appli
19	3636	99.5	695	4	US-09-548-372D-10	Sequence 10, Appl
20	3636	99.5	695	4	US-09-548-367D-10	Sequence 10, Appl
21	3636	99.5	695	4	US-09-551-853D-10	Sequence 10, Appl
22	3636	99.5	695	6	5218100-2	Patent No. 5218100
23	3630	99.4	694	1	US-08-339-152A-18	Sequence 18, Appl
24	3630	99.4	694	2	US-08-007-999B-5	Sequence 5, Appli
25	3630	99.4	694	2	US-08-689-276A-5	Sequence 5, Appli
26	3628	99.3	695	4	US-09-548-372D-12	Sequence 12, Appl
27	3628	99.3	695	4	US-09-548-367D-12	Sequence 12, Appl
28	3628	99.3	695	4	US-09-551-853D-12	Sequence 12, Appl
29	3624	99.2	695	1	US-08-371-930-27	Sequence 27, Appl
30	3624	99.2	695	5	PCT-US94-01712-27	Sequence 27, Appl
31	3612	98.9	695	1	US-08-339-152A-30	Sequence 30, Appl
32	3607	98.7	753	4	US-09-548-372D-61	Sequence 61, Appl
33	3607	98.7	753	4	US-09-548-367D-61	Sequence 61, Appl
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35	3597	98.5	751	1	US-08-123-702-4	Sequence 4, Appli
36	3597	98.5	751	2	US-08-104-165-2	Sequence 2, Appli
37	3597	98.5	751	2	US-08-422-333-2	Sequence 2, Appli
38	3597	98.5	751	2	US-08-422-333-21	Sequence 21, Appl
39	3597	98.5	751	3	US-08-464-250-2	Sequence 2, Appli
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41	3597	98.5	751	4	US-08-832-867-5	Sequence 5, Appli
42	3597	98.5	751	4	US-09-548-372D-57	Sequence 57, Appl
43	3597	98.5	751	4	US-09-548-367D-57	Sequence 57, Appl
44	3597	98.5	751	4	US-09-551-853D-57	Sequence 57, Appl
45	3597	98.5	751	6	5187153-2	Patent No. 5187153

ALIGNMENTS

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RESULT 1
US-09-548-372D-20
; Sequence 20, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-20

  Query Match             100.0%;  Score 3653;  DB 4;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-265;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDIKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDIKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTITESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 2
US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 4.9e-265;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTIESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTIESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 3
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 4.9e-265;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPIDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPIDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 4
US-09-548-372D-16
; Sequence 16, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapines
US-09-548-372D-16

Query Match 99.8%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 1.6e-264;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 5
US-09-548-367D-16
; Sequence 16, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16

; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapines
US-09-548-367D-16

Query Match 99.8%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 1.6e-264;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 6
US-09-551-853D-16
; Sequence 16, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapines
US-09-551-853D-16

Query Match 99.8%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 1.6e-264;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPITAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPITAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 7
US-09-548-372D-14
; Sequence 14, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF

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;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-14

  Query Match             99.7%;  Score 3643;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 8
US-09-548-367D-14
; Sequence 14, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-14

  Query Match             99.7%;  Score 3643;  DB 4;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 9
US-09-551-853D-14
; Sequence 14, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-14

  Query Match           99.7%;  Score 3643;  DB 4;  Length 695;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-264;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKITVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 10
US-09-548-372D-18
; Sequence 18, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-18

  Query Match           99.6%;  Score 3638;  DB 4;  Length 697;
  Best Local Similarity  99.6%;  Pred. No. 6.4e-264;
  Matches  694;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 11
US-09-548-367D-18
; Sequence 18, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-18

  Query Match           99.6%;  Score 3638;  DB 4;  Length 697;
  Best Local Similarity  99.6%;  Pred. No. 6.4e-264;
  Matches  694;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPITAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 12
US-09-551-853D-18
; Sequence 18, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-18

  Query Match           99.6%;  Score 3638;  DB 4;  Length 697;
  Best Local Similarity  99.6%;  Pred. No. 6.4e-264;
  Matches  694;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 13
US-08-123-702-2
; Sequence 2, Application US/08123702
; Patent No. 5604131
;  GENERAL INFORMATION:
;    APPLICANT:  Wadsworth, Samuel
;    APPLICANT:  Snyder, Benjamin
;    APPLICANT:  Reddy, Vermuri, B.
;    APPLICANT:  Wei, Chamer
;    TITLE OF INVENTION:  A cDNA Genomic Hybrid Sequence Encoding APP770
; Patent No. 5604131
;    TITLE OF INVENTION:  Containing a Genomic DNA Insert of the K1 and OX-2 Regions
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  GA
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/123,702
;      FILING DATE:  17-SEPT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  TSI121
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404)-873-8794
;      TELEFAX:  (404)-873-8795
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-123-702-2

  Query Match             99.5%;  Score 3636;  DB 1;  Length 695;
  Best Local Similarity   99.9%;  Pred. No. 9e-264;
  Matches  694;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 14
US-08-104-165-1
; Sequence 1, Application US/08104165
; Patent No. 5877015
;  GENERAL INFORMATION:
;    APPLICANT:  HARDY, John Anthony
;    APPLICANT:  GOATE, Alison Mary
;    APPLICANT:  MULLAN, Michael John
;    APPLICANT:  CHARTIER-HARLIN, Marie-Christine
;    APPLICANT:  OWEN, Michael John
;    TITLE OF INVENTION:  Test and Model for Alzheimer's Disease
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
```

```
;       STREET:  379 Lytton Avenue
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  US
;       ZIP:  94301
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/104,165
;       FILING DATE:  21-JAN-1992
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  9101307.8
;       FILING DATE:  21-JAN-1991
;       APPLICATION NUMBER:  9118445.7
;       FILING DATE:  28-AUG-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Liebeschuetz, Joe
;       REGISTRATION NUMBER:  37,505
;       REFERENCE/DOCKET NUMBER:  16163-000100
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326-2400
;       TELEFAX:  (415) 326-2422
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  695 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-104-165-1

  Query Match             99.5%;  Score 3636;  DB 2;  Length 695;
  Best Local Similarity   99.9%;  Pred. No. 9e-264;
  Matches  694;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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RESULT 15
US-08-464-250-1
; Sequence 1, Application US/08464250
; Patent No. 6107542
;  GENERAL INFORMATION:
;    APPLICANT:  HARDY, John Anthony
;    APPLICANT:  GOATE, Alison Mary
;    APPLICANT:  MULLAN, Michael John
;    APPLICANT:  CHARTIER-HARLIN, Marie-Christine
;    APPLICANT:  OWEN, Michael John
;    TITLE OF INVENTION:  Test and Model for Alzheimer's Disease
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,250
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/104,165
;      FILING DATE:  21-JAN-1992
;      APPLICATION NUMBER:  9101307.8
;      FILING DATE:  21-JAN-1991
;      APPLICATION NUMBER:  9118445.7
;      FILING DATE:  28-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joe
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  16163-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-250-1

  Query Match             99.5%;  Score 3636;  DB 3;  Length 695;
  Best Local Similarity   99.9%;  Pred. No. 9e-264;
  Matches  694;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db         121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy         181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

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Qy         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTITTTESVEEVVRVPTTAASTPDAV 300

Db         241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTITTTESVEEVVRVPTTAASTPDAV 300

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Db         301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Db         361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Db         421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

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Db         481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

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Db         541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

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GenCore version 5.1.6

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Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3653	100.0	697	9	US-09-794-927-20	Sequence 20, Appl
2	3653	100.0	697	9	US-09-795-847-20	Sequence 20, Appl
3	3653	100.0	697	9	US-09-794-743-20	Sequence 20, Appl
4	3653	100.0	697	9	US-09-794-748-20	Sequence 20, Appl
5	3653	100.0	697	9	US-09-794-925-20	Sequence 20, Appl
6	3653	100.0	697	9	US-09-681-442-20	Sequence 20, Appl
7	3653	100.0	697	11	US-09-869-414-20	Sequence 20, App.
8	3653	100.0	697	11	US-09-548-366-20	Sequence 20, Appl
9	3646	99.8	697	9	US-09-794-927-16	Sequence 16, Appl
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12	3646	99.8	697	9	US-09-794-748-16	Sequence 16, Appl
13	3646	99.8	697	9	US-09-794-925-16	Sequence 16, Appl
14	3646	99.8	697	9	US-09-681-442-16	Sequence 16, Appl
15	3646	99.8	697	11	US-09-869-414-16	Sequence 16, Appl
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17	3643	99.7	695	9	US-09-794-927-14	Sequence 14, Appl
18	3643	99.7	695	9	US-09-795-847-14	Sequence 14, Appl
19	3643	99.7	695	9	US-09-794-743-14	Sequence 14, Appl
20	3643	99.7	695	9	US-09-794-748-14	Sequence 14, Appl
21	3643	99.7	695	9	US-09-794-925-14	Sequence 14, Appl
22	3643	99.7	695	9	US-09-681-442-14	Sequence 14, Appl
23	3643	99.7	695	11	US-09-869-414-14	Sequence 14, Appl
24	3643	99.7	695	11	US-09-548-366-14	Sequence 14, Appl
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27	3638	99.6	697	9	US-09-794-743-18	Sequence 18, Appl
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45	3628	99.3	695	9	US-09-794-927-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-794-927-20
; Sequence 20, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AI
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-20

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  Best Local Similarity   100.0%;  Pred. No. 2.1e-226;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang

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;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-748-20

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  Best Local Similarity  100.0%;  Pred. No. 2.1e-226;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 20, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-748-20

  Query Match           100.0%;  Score 3653;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-226;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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US-09-794-925-20
; Sequence 20, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280H1
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-794-925-20

  Query Match           100.0%;  Score 3653;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-226;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 6
US-09-681-442-20
; Sequence 20, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-681-442-20

  Query Match           100.0%;  Score 3653;  DB 9;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-226;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVIPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 7
US-09-869-414-20
; Sequence 20, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-869-414-20
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  Query Match           100.0%;  Score 3653;  DB 11;  Length 697;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-226;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 8
US-09-548-366-20
; Sequence 20, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
;  TITLE OF INVENTION:  USES THEREFOR
;  FILE REFERENCE:  28341/6280A
;  CURRENT APPLICATION NUMBER: US/09/548,366
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
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;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;    LENGTH: 697
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-548-366-20

  Query Match             100.0%;  Score 3653;  DB 11;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-226;
  Matches  697;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTIESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTIESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
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Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVIPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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Db        661 VEVDAAVIPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 9
US-09-794-927-16
; Sequence 16, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/794,927
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,233
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;    LENGTH: 697
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-794-927-16

  Query Match             99.8%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity   99.9%;  Pred. No. 5.8e-226;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||| |||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 10
US-09-795-847-16
; Sequence 16, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-795-847-16

  Query Match           99.8%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 5.8e-226;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTIAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 11
US-09-794-743-16
; Sequence 16, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;  LENGTH: 697
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-794-743-16

  Query Match           99.8%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 5.8e-226;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 12
US-09-794-748-16
; Sequence 16, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-16

Query Match 99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTIVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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RESULT 13
US-09-794-925-16
; Sequence 16, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73

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;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-925-16

  Query Match            99.8%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 5.8e-226;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDIKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
              |||||||||||||||||||||||||||||||||||||
Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697


RESULT 14
US-09-681-442-16
; Sequence 16, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-681-442-16

  Query Match            99.8%;  Score 3646;  DB 9;  Length 697;
  Best Local Similarity  99.9%;  Pred. No. 5.8e-226;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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RESULT 15
US-09-869-414-16
; Sequence 16, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-869-414-16

Query Match 99.8%; Score 3646; DB 11; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTITTESVEEVVRVPTTAASTPDAV 300
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Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Search completed: October 2, 2003, 14:18:39
Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:04 ; Search time 16.6667 Seconds
(without alignments)
4021.774 Million cell updates/sec

Title: US-09-806-194-20
Perfect score: 3653
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3636	99.5	695	1	A49795	Alzheimer's diseas
2	3585.5	98.2	770	1	QRHUA4	Alzheimer's diseas
3	3539	96.9	695	2	S00550	Alzheimer's diseas
4	3514	96.2	695	2	A27485	Alzheimer's diseas
5	3098	84.8	747	2	JH0773	Alzheimer's diseas
6	2105	57.6	484	4	A32761	hypothetical Alzhe
7	1723	47.2	763	2	A49321	amyloid beta (A4)
8	1711	46.8	765	2	S42880	amyloid precursor-
9	1699	46.5	751	2	A49974	beta-amyloid precu
10	1180	32.3	653	2	A46362	amyloid precursor-
11	1138	31.2	511	2	JC1404	CDEI-box DNA-bindi
12	816.5	22.4	686	2	T15795	hypothetical prote
13	754	20.6	886	2	A32758	beta-amyloid-like
14	706	19.3	246	2	S38344	CDEI-binding prote
15	406	11.1	82	2	PQ0438	Alzheimer's diseas
16	291.5	8.0	191	2	A35981	sperm membrane pro
17	278	7.6	57	2	E60045	Alzheimer's diseas
18	278	7.6	57	2	F60045	Alzheimer's diseas
19	278	7.6	57	2	G60045	Alzheimer's diseas
20	278	7.6	57	2	D60045	Alzheimer's diseas
21	278	7.6	57	2	A60045	Alzheimer's diseas
22	278	7.6	57	2	B60045	Alzheimer's diseas
23	217	5.9	42	2	PN0512	beta-amyloid prote
24	192.5	5.3	1110	2	I51116	NF-180 - sea lampr
25	185.5	5.1	407	1	EDBEQ3	immediate-early pr
26	184	5.0	5170	2	T15348	hypothetical prote
27	182	5.0	522	2	T32444	hypothetical prote
28	180.5	4.9	993	2	S49461	synaptonemal compl
29	179.5	4.9	1188	2	T46608	zinc finger protei
30	175.5	4.8	802	1	S48529	NAB3 protein - yea
31	174.5	4.8	464	2	H90279	microtubule bindin
32	174.5	4.8	884	2	T20405	hypothetical prote
33	174	4.8	579	2	JH0820	160K golgi antigen
34	174	4.8	1087	2	T30330	gelsolin-related p
35	174	4.8	1271	2	A45555	glutamate rich pro
36	173.5	4.7	793	1	JH0628	caldesmon - human
37	173	4.7	1187	2	T46637	transcription fact
38	172	4.7	771	1	A33430	h-caldesmon - chic
39	172	4.7	784	2	PN0009	neurofilament trip
40	172	4.7	1182	2	T30189	myelin transcripti
41	169.5	4.6	298	1	TPHUTC	troponin T, cardia
42	169.5	4.6	721	2	S29795	hypothetical prote
43	169	4.6	885	2	G71608	ATP-dept. acyl-CoA
44	168.5	4.6	675	2	T03744	myoD protein inhib
45	168.5	4.6	913	2	T52485	neurofilament prot

ALIGNMENTS

RESULT 1
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human suppor
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote
C;Keywords: alternative splicing

Query Match 99.5%; Score 3636; DB 1; Length 695;
Best Local Similarity 99.9%; Pred. No. 3.7e-184;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
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Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
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RESULT 2
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A39384; S29075; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The ProA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
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A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral h
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Al
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; And
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; M
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds fo
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik,
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovasc
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
```

A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for resid
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for resi
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuth

Query Match 98.2%; Score 3585.5; DB 1; Length 770;
Best Local Similarity 90.0%; Pred. No. 1.9e-181;
Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;

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Qy          1 MLPGLALLLLAAWTARALEVPIDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
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Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTIQEPLARD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
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Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||.||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
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Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
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Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYISIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 3
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg,
EMBO J. 7, 1365-1370, 1988

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A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brai
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
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Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||:|||||||||||||||||||||||||||||| | ||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
              ||:|||| |||||||||||||||||||||'|||||||||||||||||||||||||||||||
Db        241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPITAASTPDAV 300

Qy        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
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Db        301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
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Db        361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHHVFNMLK 420

Qy        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
              |||:||||:|||||:|||||||||||||||||||||||||:|||||:|||||||||||||
Db        421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
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Db        481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy        541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLITRPGSGLTNIKTEEISEVKMDAEF 600
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Db        541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy        601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
              ||||:|| |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
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Db        661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 4
A27485
A;Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzhe
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
C;Keywords: alternative splicing; amyloid; transmembrane protein

  Query Match            96.2%;  Score 3514;  DB 2;  Length 695;
  Best Local Similarity  96.7%;  Pred. No. 9.9e-178;
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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| |||||||||||||||||||||:|||||||||||:|:|||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||:|||||||||||||||||||||||||||||| | ||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
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Db        181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWVGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASIPDAV 300
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RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 84.8%; Score 3098; DB 2; Length 747;
Best Local Similarity 80.9%; Pred. No. 8.7e-156;
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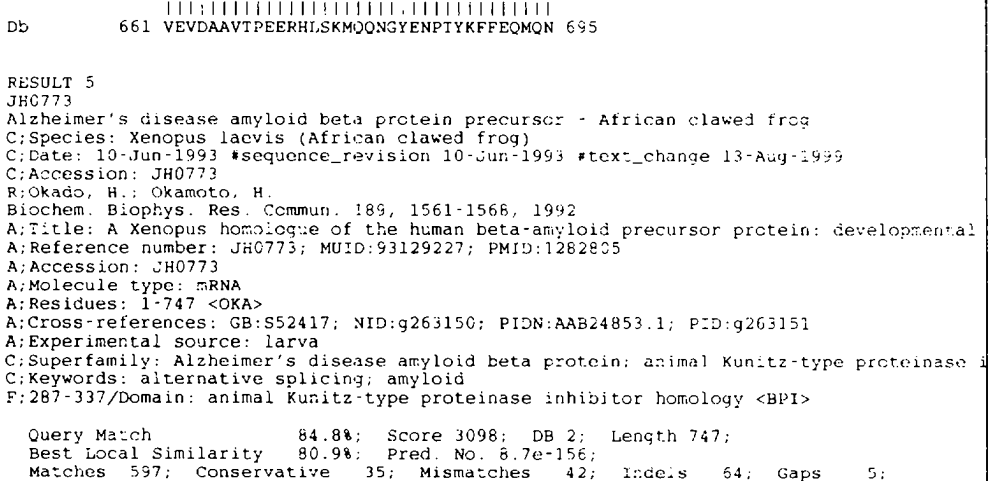
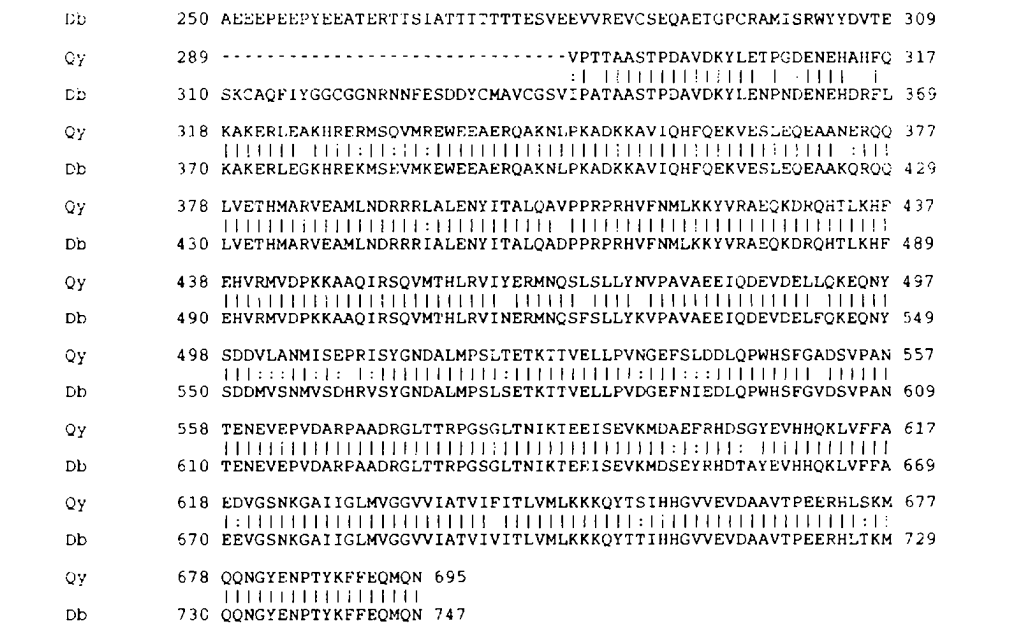
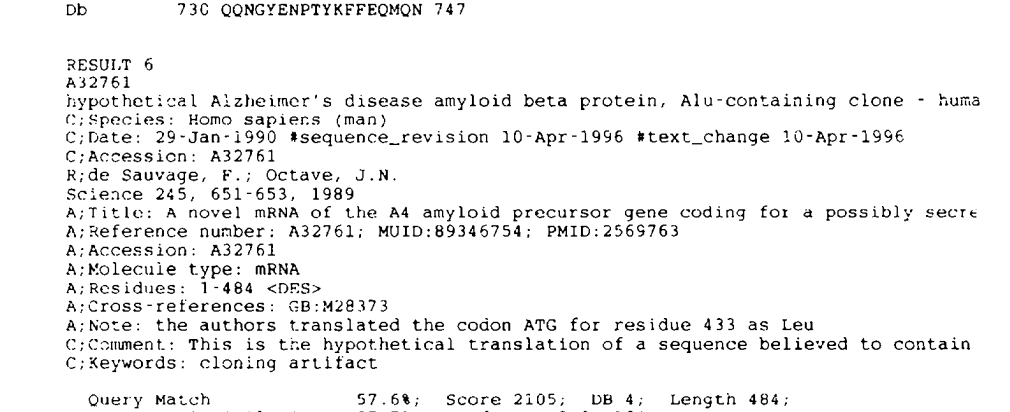




RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - huma
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C;Accession: A32761
R;de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A;Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secre
A;Reference number: A32761; MUID:89346754; PMID:2569763
A;Accession: A32761
A;Molecule type: mRNA
A;Residues: 1-484 <DES>
A;Cross-references: GB:M28373
A;Note: the authors translated the codon ATG for residue 433 as Leu
C;Comment: This is the hypothetical translation of a sequence believed to contain
C;Keywords: cloning artifact

Query Match 57.6%; Score 2105; DB 4; Length 484;
Best Local Similarity 87.7%; Pred. No. 9.9e-104;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;



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Qy        289 ------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 323
                                      :|||||||||||||||||||||||||||||||||||
Db        241 FYGGCGGNRNNFDTEEYCMAVCGSAIPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 300

Qy        324 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM 383
              |||||||||||||||||||||,|||||||||||||:|||||||||||||||||||| |||||
Db        301 EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM 360

Qy        384 ARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 443
              |||'||||||||||||||||||,|||||||||||||:||||:||||,|||||||||| ||||||
Db        361 ARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV 420

Qy        444 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV 487
              ,|||||:|||||||,|||:|||||||||||||:|||||:||||:|
Db        421 DPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV 464


RESULT 7
A49321
amyloid beta (A4) homolog 2 precursor - human
N;Alternate names: CDEI-binding protein
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49321; S34644; S40519
R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
A;Reference number: A49321; MUID:93250009; PMID:8485127
A;Accession: A49321
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <SPR>
A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)
A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A;Description: The human homologue of the murine CDEI binding protein is an amyloid prec
A;Reference number: S34644
A;Accession: S34644
A;Molecule type: mRNA
A;Residues: 1-763 <VON>
A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A;Reference number: S40519; MUID:94035131; PMID:8220435
A;Accession: S40519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <WAS>
A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C;Genetics:
A;Gene: GDB:APLP2; APPL2
A;Cross-references: GDB:139159; OMIM:104776
A;Map position: 11q23-11q25
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; transmembrane protein
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             47.2%;  Score 1723;  DB 2;  Length 763;
  Best Local Similarity   47.0%;  Pred. No. 2.3e-83;
  Matches  371;  Conservative  112;  Mismatches  166;  Indels  140;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | ||||   :| || :         |||    :|||||||||||:||||:|:| |||: ||
Db         15 LLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKICIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:r :||| :||||||:|||||||||||:|||| ::| || :| :||||:   || |::
Db         75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132
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```
Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||||||||| ||||:||:| |:|||:||| | ||||| || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|||| :  :|  : |||:       : :  |  || |  :|    |:
Db        193 DQFHGTEYVCCPQTK11GSVSKEEEEEDEE-------EEEEDEEEDYDVYKSEEPTEAD 245

Qy        237 VEE--EEA--DDDEDDEDGDEVEEEAEEPY----------EEATERTISIATTTTTTTES 282
              ::  | }  :||||:|:|:|| |: :  |          |  ||  :    :    |
Db        246 LEDFTEAAVDEDDEDEEEGEEVVEDRDYYYDIFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy        283 VEEV-------------------------------------------------VRVP 290
              |: |                                                  :|
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMIP 365

Qy        291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPK 350
              |   | | || ; ||  |:|||| ||||||:|| :|| || :| :|||||| |||||||
Db        366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy        351 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPP 410
              |::: :|||||  |:::|:|||:|:|||||||:|||||||||||||:|||||: |||: ||
Db        425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP 484

Qy        411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 470
              ||  :  |::|||| ||| ||:::|::||  |||:||||:::|:|||| |; || |||
Db        485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSL 544

Qy        471 SLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVE 530
              |||| || ||:|||:|:||||||:::       |:|          |    |::|    |
Db        545 SLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTASISETPVDVR 587

Qy        531 LLPVNGEFSLDDLQPWHSFGADSVPANIENEVEPVDARPAADRGLTTRPGSGLTN----- 585
              |: | | ::: |:| |      ||  |||    | :|      :  : |||:
Db        588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGGL 635

Qy        586 IKIEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKG 625
              |  ||    |: |:|      |   :|  ::::| || ||                  :
Db        636 IGAEEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEEERESVGPLREDFSLSSS 693

Qy        626 AIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENP 685
              |:|||:|  | ||||| |:||||:|:|| :| ||:|||  :|||||||:||| :|||||
Db        694 ALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENP 753

Qy        686 TYKFFEQMQ 694
              |||: |||
Db        754 TYKYLEQMQ 762


RESULT 8
S42880
amyloid precursor-like protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S42880; S47528
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A;Description: Complete nucloetide ad deduced amino acid sequence of rat amyloid pr
A;Reference number: S42880
A;Accession: S42880
A;Molecule type: mRNA
A;Residues: 1-765 <SAN>
A;Cross-references: EMBL:X77934
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid proteir
A;Reference number: S47528; MUID:94368849; PMID:8086458
A;Accession: S47528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-765 <SA2>
A;Cross-references: EMBL:X77934
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteir
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C;Keywords: alternative splicing
F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.8%; Score 1711; DB 2; Length 765;
Best Local Similarity 46.1%; Pred. No. 9.8e-83;
Matches 363; Conservative 122; Mismatches 167; Indels 136; Gaps 20;

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Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              : :|||   || |  :          |||    :|||||||||||:||||:|:| |||: ||
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :|||||||||||||:|||||, | :,|:| :||||:  : ||||:
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||||||||| |||| |:| ||||:|||  |  |||| || |  :   |: ||| ||||:
Db        133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYA-DGSEDKVVEVAEEEE 233
              |:| | |:|||| :  :||:  | : ||:: :      : ||| | ||         |:
Db        193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEE----DEEEDYALDKSEFPTEADLEDFT 248

Qy        234 VAEVEEEEADDDEDDEDGDEVEEEAEEPYEE------ATERTISIATTITTTTESVEEVV 287
              |  :|:| :::|:::|:|:|| |: :  |:         !  |  ::  | : : :   |
Db        249 EAAADEDEDEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV 308

Qy        288 R-------------------------------------------------------VPT 291
              :                                                       :|
Db        309 KAVCSQEAMIGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMIPP 368

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
              |   | | || | ||  |:|||| ||||||:|| :.| || :| :|||||| |.|||:||
Db        369 TPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRSRMDRVKKEWEEAELQAKNLPKA 427

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
              ::: :,|||| |::|:|:||:|:|::|||||:||||:|||||||:|:|||:: |::: ||
Db        428 ERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYLAALQSDPPR 487

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
              |  :   |::||'|| |'| ||::|::|  |||:||||::|:|||| || || |||||
Db        488 PHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSLS 547

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
              ||| || ||:|||:|:|||||::       |:|         '    |:::|     .
Db        548 LLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSSISENPVDVR- 589

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN-----I 586
              |: | | ::: :|| |     |: :|'|    ' :|    :  : |||:       |
Db        590 --VSSEES-EEIPPFHPF--HPFPSLSENE----DTQPELYHPM--KKGSGMAEQDGGLI 638

Qy        587 KTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKGA 626
              '|    |: |||     |   :|  ::::| '| ||                     :
Db        639 GAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPDSVGPLREDFSLSSSA 696

Qy        627 IIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPT 686
              :|||:|  | ||||| |:||||:|:|| :| ||:|:|   :|||||||:'|| :||||||
Db        697 LIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPMLTPEERHLNKMQNHGYENPT 756

Qy        687 YKFFEQMQ 694
              ||: ||||
Db        757 YKYLEQMQ 764
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RESULT 9
A49974
beta-amyloid precursor protein 2 homolog APLP2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49974
R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
A;Reference number: A49974; MUID:94132029; PMID:8300594
A;Accession: A49974
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-751 <SLU>
A;Cross-references: GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558468
A;Note: sequence extracted from NCBI backbone (NCBIP:144636)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.5%; Score 1699; DB 2; Length 751;
Best Local Similarity 45.8%; Pred. No. 4.1e-82;
Matches 362; Conservative 113; Mismatches 160; Indels 156; Gaps 20;

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Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              : :|||   || |  :          |||    :|||||||||||:||||:|:| |||: ||
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :|||||||||||||:|||||| | :||:| ::||':  | ||||::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||||| ||||| |:| |||||:||| |  |||: || |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE---E 231
              |:| | |:|||| :  :|||:  | : ||::          |  |  ||  :: :|  /
Db        193 DQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEFPTE 243

Qy        232 EEVAEVEEEEAD-DDEDDEDGDEVEEE-------------AEEPYEEATERTTSIATTT 276
              :: :  |  || ::||:|:|:|| |:               | | | ::| | |
Db        244 ADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNEENPTEPSSEGTIS----- 298

Qy        277 TTTTESVEEV---------------------------------------------------- 286
                    | | :|
Db        299 --DKEIVHDVKAVCSQEAMIGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYC 356

Qy        287 -----VRVPITAASIPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
                  :| |   | | || | ||  |:|||| ||||||:|| :|| || :| :|||||
Db        357 MAVCKAMIPPIPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEA 415

Qy        342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENY 401
              | ||||||| ::: :|||||  |::||:|||:|:|||||||:|||||||||||:|||||
Db        416 ELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENY 475

Qy        402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
              : |||: |||'  :   |::|||||| ||| ||::|::||  |||:|||||||||||' |
Db        476 LAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHV 535

Qy        462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 521
              | || |||||||| || ||:|||:|:||||||:::       |:|          |    |
Db        536 IEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSS 578

Qy        522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGS 581
              ::|    | :      | :    | | |      |: :|||            |:  : |
Db        579 ISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQDG- 621

Qy        582 GLTNIKTEE1-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------N 623
              ||   : : | :: |||     |   :|  ::::| || ||                  :
Db        622 GLIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFSLS 679

Qy        624 KGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYE 683
              |:|||:|  | ||||| |:||||:|:|| :| ||:|||  :|||||||:||| :|||
Db        680 SNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYE 739

Qy        684 NPTYKFFEQMQ 694
              ||||||: ||||
Db        740 NPTYKYLEQMQ 750
```

RESULT 10
A46362

```
amyloid precursor-like protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A46362
R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
A;Title: Identification of a mouse brain cDNA that encodes a protein related to the Alz
A;Reference number: A46362; MUID:93066322; PMID:1279693
A;Accession: A46362
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-653 <WAS>
A;Experimental source: brain
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118584)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: transmembrane protein

  Query Match            32.3%;  Score 1180;  DB 2;  Length 653;
  Best Local Similarity  38.4%;  Pred. No. 7.3e-55;
  Matches  269;  Conservative  121;  Mismatches  232;  Indels   78;  Gaps   17;

Qy          1 MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGT 59
              :|| |:|||| |  |   | . :   |      :|  :||| :| ::: |:|: |:  :
Db         22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy         60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
              : ::   : :|:| :::|||| |  | :| | : :: ':|   |     :|   |::: |:
Db         81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAIPMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy        119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
              ||||:|||||: |:|:|||||: ||:    |  |:: || :  |:  |||: || ::
Db        141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDR 200

Qy        179 FRGVEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
              |||||:|||||    : :     | :  :  : ||     |:| ||       |:||
Db        201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-------EEEVESF 248

Qy        238 EEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
              :  |  :  :| ||| ||     :  | : :  | ||     |:| ||       |:||
Db        249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR--------PT------ 294

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              | :| |   ||:  ||  | :||  ||  :  :::|||||  |: |:|||| ||:::|:
Db        295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              :|||  :::||:: : |||:|||||  || |::||:||  :|| :: |||  ||:  |
Db        355 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |:::|||||:::|||:|::||  |||:|| |:| || |||:|: ||||:|| ||   |
Db        415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
              :|:|:: :: |||           ||  :   :    || :| | :| :
Db        475 HLAQELRPQIQELL----------LAEHLGPSEL----DASVPGSSSEDK---------- 510

Qy        537 EFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
                  |||              |:: :|    |   :' | : |     |   : : :
Db        511 ----GSLQP-----------PESKDDPPVTLP---KGSTDQPSSSSGREKLTPLEQYEQ 551

Qy        597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVML-KKKQ 652
                 |:  |    |:         | :: |: |:: |    :::| ::|:::| |||
Db        552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSLIVLSLLLLRKKKP 611

Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
              | :| ||||||;  :| ||: | ::|::||||||:| |:
Db        612 YGTISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 651


RESULT 11
JC1404
```

```
CDEI-box DNA-binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C;Accession: JC1404
R;Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
A;Title: A murine sequence-specific DNA binding protein shows extensive local simi
A;Reference number: JC1404; MUID:93129193; PMID:1482349
A;Accession: JC1404
A;Molecule type: mRNA
A;Residues: 1-511 <VID>
C;Comment: This protein plays an important role in the early development of the mo
C;Keywords: DNA binding; transmembrane protein

  Query Match            31.2%;  Score 1138;  DB 2;  Length 511;
  Best Local Similarity  45.6%;  Pred. No. 8.8e-53;
  Matches  252;  Conservative   92;  Mismatches  129;  Indels   80;  Gaps   16;

Qy        174 CGIDKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE- 230
              ||:|:| | |:|||| : :|||: | : ||::           | |  ||  :: :|
Db          6 CGVDQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEF 56

Qy        231 --EEEVAEVEEEEAD-DDEDDEDGDEVEEEAE--------EPYEEATERTTSIATTTTTT 279
                | :: :  |  || ::||:|:|:|| |: :          : | |  |  |  ::  | :
Db         57 PIEADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTIS 114

Qy        280 TESVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWE 339
                :  :   |:|| |   | | || | ||  |:|||| ||||||:|| :|| || :| :|||
Db        115 DKEIVHDVKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWE 173

Qy        340 EAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALE 399
              ||| ||||||| ::: :|||||  |::||:||::|:|||||||:|'|:|||||'||:|||
Db        174 EAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALE 233

Qy        400 NYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHL 459
              ||: |||: |||| :   ::|||||| ||| |::|:::|  |||:|||'::|||||||
Db        234 NYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHL 293

Qy        460 RVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALM 519
              || || |||||||| || ||:|||:|:|||||:::      |:|          |
Db        294 HVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFT 336

Qy        520 PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRP 579
              |:::|    | :    | :    | | |     |: :|||                |:  :
Db        337 SSISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQD 380

Qy        580 GSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS---------------- 622
              | ||   : : | |: |||     |   :|  ::::| || ||
Db        381 G-GLIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFS 437

Qy        623 -NKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNG 681
               :  |:|||:|  | ||||| |:||||:|:|| :| ||:|||  :|||||||:||| :|
Db        438 LSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHG 497

Qy        682 YENPTYKFFEQMQ 694
              |||||||: ||||
Db        498 YENPTYKYLEQMQ 510


RESULT 12
T15795
hypothetical protein C42D8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C;Accession: T15795; A49414
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C42D8.
A;Reference number: Z18405
A;Accession: T15795
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-686 <HAL>
```

A;Cross-references: EMBL:U56966; NID:g1293844; PID:g1293850; PIDN:AAA98722.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone C42D8
R;Daigle, I.; Li, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993
A;Title: apl-1, a Caenorhabditis elegans gene encoding a protein related to the human be
A;Reference number: A49414; MUID:94089766; PMID:8265668
A;Accession: A49414
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-686 <DAI>
A;Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297
C;Genetics:
A;Gene: CESP:C42D8.8
A;Map position: X
A;Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 580/3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

Query Match 22.4%; Score 816.5; DB 2; Length 686;
Best Local Similarity 29.1%; Pred. No. 1.1e-35;
Matches 222; Conservative 110; Mismatches 275; Indels 155; Gaps 22;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              :: || : :| | |  }   |           | :  ||  | :|  : | | :|
Db          6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKIDDERYA 63

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               ||   |  |:|:||:: || : |||:|| :  |:| ::|:     ||   | | || |: |
Db         64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WIHSVRPYHCIDG 122

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN------LHDYGMLLPC 174
               || |:|| ||  |:| '   | |  : |:   | : ;  | :        :  : :| |
Db        123 EPHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy        175 GIDKFRGVEFVCCPLAEFSDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV 234
               :| | ||||||||    :|  :  | ::
Db        183 ALDMFTGVEFVCCP----NDQTNKIDVQKTK---------------------------- 209

Qy        235 AEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAA 294
                 |:|: ||||:|    :|  :  ||:::|  ||
Db        210 ---EDEDDDDDEDDAYEDDYSEESDEKDEE---------------------------- 236

Qy        295 STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA-----ERQAKNLP 349
               | : | | :     |:|  |:||: |:: ;|!::: :||:|| :     |:::|:: |
Db        237 -EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHRKKVDKVMKEWGDLETRYNEQKAKD-P 294

Qy        350 KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL- 405
               |  :|     :|: | |:|:|    |:::   |  |!:|||||:::| |  :|  !!
Db        295 KGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA 354

Qy        406 -QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE 464
                   |    |   :| |:|||:||| |||  : |:     |:||  :  |:  || |
Db        355 THVNKPNKHSVLQSLKAYIRAEEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL 414

Qy        465 RMNQSLSLLYNVP---------AVA--EEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
               |:| :|:::| : |         ||   :: :|||   :  |    |  |  :| :   |
Db        415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE----DSELTPITHDDEFSK 470

Qy        514 GN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANT---ENEVEP 564
                  |   |: |     :     ::||     | ::   ::    |      |    : :|:
Db        471 NAKLDVKAPTTTAKPVKETDNAKVLPTEASDSEEEADEYYEDEDDEQVKKTPDMKKKVKV 530

Qy        565 VDARP---------------------AADRGLTTRPGSGLINIKTEE-----ISEVKMDA 598
               || :|                     |       |  |: :::|     | |::::|
Db        531 VDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSSESDEDEDKNIKELRVDI 590

Qy        599 E---------FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLK 649
               |         :|||        ||:   |  |        ::   :  | | |    :
Db        591 EPIIDEPASFYRHD--------KLIQSPEVERSASSVFQPYVLASAMFITAICIIAFAIT 642

Qy        650 KKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
                :      | :|||   |||||:: || ||||||| ||:
Db        643 NARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFFD 683
```

RESULT 13
A32758
beta-amyloid-like protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 24-Sep-1998
C;Accession: A32758
R;Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989
A;Title: A Drosophila gene encoding a protein resembling the human beta-amyloid pr
A;Reference number: A32758; MUID:89184650; PMID:2494667
A;Accession: A32758
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-886 <ROS>
A;Cross-references: GB:J04516; NID:g158371; PID:g158372
C;Genetics:
A;Gene: FlyBase:Appl
A;Cross-references: FlyBase:FBgn0000108
C;Keywords: transmembrane protein

Query Match 20.6%; Score 754; DB 2; Length 886;
Best Local Similarity 25.7%; Pred. No. 2.9e-32;
Matches 234; Conservative 127; Mismatches 287; Indels 264; Gaps 29;

```
Qy          7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDSDPSG 58
              ||| : |   |:      | | : |     |||||: |  |::      : : |:| :| |
Db          9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVTDLSK 63

Qy         59 T---KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
                 ||:  |  :| |||:: ||   |||:||::    |  ||:::|     :||    ::
Db         64 KTIGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWI 123

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
               |:||| | | ||||||: | | |       |   : |:      | |:   :  : :|| |
Db        124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRTFAMLL 182

Qy        173 PCGIDKFRGVEFVCCP-----------------------------LAEESDNVD---SA 199
               ||||  | ||||:|||                             : :| |: |   |
Db        183 PCGISVFSGVEFVCCPKHFKTDEIHVKKTDLPVMPAAQINSANDELMNDEDDSNDSNYSK 242

Qy        200 DAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV----------------------AEV 237
               || ||| |      | |   | :::   ||:|                         ||
Db        243 DANEDDLD------DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINAEY 296

Qy        238 EE-EEADDDEDDEDGDEVEEEAEEPY--------------------------EEATERT 269
               :  || |: |:|  | | | | |  :                          |:|  ::
Db        297 DSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLKSDSSSPSSAPVAPAPEKAPVKS 356

Qy        270 TSIATTTTTTTESVEEVV-----------RVPTTAASTPDAVDKYLETPGDENEHAHFQK 318
               !: :|   :  :   |               |:!|  |    | |         ||  ::
Db        357 ESVTSTPQLSASAAAFVAANSGNSGIGAGAPPSTAQPTS---DPYFTHFDPHYEHQSYKV 413

Qy        319 AKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKA-------VIQHFQEKVESLEQEA 371
               :::|||  |||:::::||::| : | : :::  || ||       :   ||  |::||:|
Db        414 SQKRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFKQRMTARFQTSVQALEEEG 473

Qy        372 ANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQ 431
               ||: ||   |  || | | :| |:|  |:  |  ||   ||   ||   |:| ::|  |||
Db        474 NAEKHQLAAMHQQRVLAHINQRKREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDRA 533

Qy        432 HTLKHFEH-VRMVDP---KKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI---- 483
               | | |: | :    |   : ||  | : :  /  |   :|||:::|   | :: :|
Db        534 HALAHYRHLLNSGGPGGLEAAASERPRTLERLIDIDRAVNQSMTMLKRYPELSAKIAQLM 593

Qy        484 ---------QDEV---------------------------------------------- 487
                        :|::
Db        594 NDYILALRSKDDIPGSSLGMSEEAEAGILDKYRVEIERKVAEKERLRLAEKQRKEQRAAE 653

Qy        488 -----DELLQKEQNYSDDVLANMISE----------------------PRISYGNDALM 519
                    :| |: |    ||:| : ::|                        |   | || :
Db        654 REKLREEKLRLEAKKVDDMLKSQVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAAL 713
```

```
Qy        520 -----PSLTETKTIVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRG 574
                   |:|  ||:         |  | | :  ' :|  :|       | |     |  |
Db        714 VTAANPNLETTKS---------EKDLSDTE----YGEATVSTTKVQTVLPTVDDDAVQRA 760

Qy        575 LTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---GA 626
              :    :         ::  : : : :|   ::: |::  |     ||:   : !
Db        761 VEDVAAA---------VAHQEAEPQVQHFMTHDLGHRESSFSLRREFAQHAHAAKEGRNV 811

Qy        627 IIGLMVGGVVIATVIFITLVMLKKKQYTSIH-HGVVEVDAAVTP------EERHLSKMQQ 679
                 :  |: :   :|: : : | :   | :  | :' |  |:        ||: :  ||
Db        812 YFTLSFAGIALMAAVFVGVAVAKWRISRSPHAQGFIEVDQNVITHHPIVREEKIVPNMQI 871

Qy        680 NGYENPTYKFFE 691
              || ||||| :||
Db        872 NGYENPTYKYFE 883


RESULT 14
S38344
CDEI-binding protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1996
C;Accession: S38344
R;Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.
Biochim. Biophys. Acta 1216, 154-156, 1993
A;Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
A;Reference number: S38344; MUID:94032480; PMID:8218408
A;Accession: S38344
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-246 <HAN>
A;Cross-references: EMBL:Z22592
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

  Query Match             19.3%;  Score 706;  DB 2;  Length 246;
  Best Local Similarity   51.5%;  Pred. No. 2e-30;
  Matches  136;  Conservative   35;  Mismatches   51;  Indels   42;  Gaps    7;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSD 56
              | :|||   || |  :       |||    :|||||'| |:|||||:':| ;;|: ;|
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :|||||||:||||:|||||:|||||| | :||:| ::|||:    ||.::
Db         75 TGIKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              ||||||||| ||||| |:| |:|||:|:| |  |:|: .| |  :   |: |||||.|:
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
              |:| | |:|||   ::  |||                    | :   |||:
Db        193 DQFHGTEYVCCP---QTKTVDS----------------------DSTMSKEEEEE--- 222

Qy        237 VEEEEADDDED-DEDGDEVEEEAE 259
               ||:| |::|| | |  |   ||:
Db        223 -EEDEEDEEEDYDLDKSEFPTEAD 245


RESULT 15
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83557
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteir
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

  Query Match             11.1%;  Score 406;  DB 2;  Length 82;
  Best Local Similarity   98.8%;  Pred. No. 3.1e-15;
  Matches   81;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        581 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATV 640
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATV 60

Qy        641 IFITLVMLKKKQYTSIHHGVVE 662
              | |||.|||||:||||||||
Db         61 IVITLVMLKKKQYTSIHHGVVE 82


Search completed: October 2, 2003, 14:00:36
Job time : 19.5667 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:24 ; Search time 10 Seconds
(without alignments)
3277.761 Million cell updates/sec

Title: US-09-806-194-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3585.5	98.2	770	1	A4_HUMAN	P05067 h amyloid b
2	3585.5	98.2	770	1	A4_MACFA	P53601 m amyloid b
3	3579	98.0	751	1	A4_SAISC	Q95241 s amyloid b
4	3530.5	96.6	770	1	A4_PIG	P79307 s amyloid b
5	3517.5	96.3	770	1	A4_CAVPO	Q60495 c amyloid b
6	3488.5	95.5	770	1	A4_MOUSE	P12023 m amyloid b
7	3488.5	95.5	770	1	A4_RAT	P08592 r amyloid b
8	1730	47.4	695	1	APP2_MOUSE	Q06335 mus musculu
9	1723	47.2	763	1	APP2_HUMAN	Q06481 homo sapien
10	1711	46.8	765	1	APP2_RAT	P15943 rattus norv
11	1185	32.4	650	1	APP1_HUMAN	P51693 homo sapien
12	1180	32.3	653	1	APP1_MOUSE	Q03157 mus musculu
13	816.5	22.4	686	1	A4_CAEEL	Q10651 caenorhabdi
14	755.5	20.7	887	1	A4_DROME	P14599 drosophila
15	287	7.9	59	1	A4_BOVIN	Q28053 bos taurus
16	283	7.7	58	1	A4_RABIT	Q28748 oryctolagus
17	283	7.7	58	1	A4_SHEEP	Q28757 ovis aries
18	282	7.7	58	1	A4_CANFA	Q28280 canis famil
19	278	7.6	57	1	A4_URSMA	Q29149 ursus marit
20	185.5	5.1	407	1	IE68_HSVSA	Q01042 herpesvirus
21	180.5	4.9	993	1	SCP1_MOUSE	Q62209 mus musculu
22	176	4.8	2004	1	MOZ_HUMAN	Q92794 homo sapien
23	175.5	4.8	802	1	NAB3_YEAST	P38996 saccharomyc
24	174	4.8	579	1	G160_HUMAN	Q08378 homo sapien
25	173.5	4.7	793	1	CALD_HUMAN	Q05682 homo sapien
26	172	4.7	771	1	CALD_CHICK	P12957 gallus gall
27	169.5	4.6	297	1	TRT2_HUMAN	P45379 homo sapien
28	169.5	4.6	721	1	YCF2_OENPI	P31568 oenothera p
29	168.5	4.6	1875	1	MLP1_YEAST	Q02455 saccharomyc
30	168	4.6	1240	1	YNJ1_YEAST	P53935 saccharomyc
31	167.5	4.6	1976	1	MYHA_HUMAN	P35580 homo sapien
32	166.5	4.6	816	1	YG3A_YEAST	P53278 saccharomyc
33	166.5	4.6	1976	1	MYHA_RAT	Q9jlt0 rattus norv
34	164.5	4.5	1325	1	G160_MOUSE	P55937 mus musculu
35	163.5	4.5	681	1	MP10_HUMAN	O00566 homo sapien
36	162.5	4.4	712	1	NUCL_RAT	P13383 rattus norv
37	162	4.4	2017	1	MYSN_DROME	Q99323 drosophila
38	160.5	4.4	1976	1	MYHA_BOVIN	Q27991 bos taurus
39	160	4.4	694	1	NUCL_CHICK	P15771 gallus gall
40	159.5	4.4	1955	1	PUMA_PARUN	O61308 parascaris
41	158	4.3	301	1	TRT2_CHICK	P02642 gallus gall
42	157.5	4.3	706	1	NUCL_HUMAN	P19338 homo sapien
43	156.5	4.3	5596	1	MDN1_HUMAN	Q9nu22 homo sapien
44	156	4.3	1332	1	SPI7_YEAST	P35177 saccharomyc
45	156	4.3	1433	1	REST_CHICK	O42184 gallus gall

ALIGNMENTS

RESULT 1
A4_HUMAN
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q9BT38;
AC Q9UCB6; Q9UQ58;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";

RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [10]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [11]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [12]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [15]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [16]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [17]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [18]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [19]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [20]
RP SEQUENCE OF 672-681.
RC TISSUE=Brain cortex;
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [21]
RP SEQUENCE OF 674-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease.";

```
  Query Match             98.2%;  Score 3585.5;  DB 1;  Length 770;
  Best Local Similarity   90.0%;  Pred. No. 1.7e-170;
  Matches  693;  Conservative    1;  Mismatches    1;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADIDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                  :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 2
A4_MACFA
ID   A4_MACFA        STANDARD;       PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
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CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -6 or -8
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1    17       BY SIMILARITY.
FT   CHAIN        18   770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18   687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18   671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672   770       C99 (POTENTIAL).
FT   CHAIN       672   713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       672   711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       688   770       C83 (POTENTIAL).
FT   CHAIN       688   713       P3(42) (POTENTIAL).
FT   CHAIN       688   711       P3(40) (POTENTIAL).
FT   CHAIN       712   770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       714   770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       721   770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       740   770       C31 (POTENTIAL).
FT   DOMAIN       18   699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700   723       POTENTIAL.
FT   DOMAIN      724   770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96   110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181   188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291   341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391   423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491   522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523   540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732   751       INTERACTION WITH G(O)-ALPHA
FT                               (BY SIMILARITY).
FT   DOMAIN      230   260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274   280       POLY-THR.
FT   SITE        144   144       REQUIRED FOR COPPER(II) REDUCTION
FT                               (BY SIMILARITY).
FT   ACT_SITE    301   302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671   672       CLEAVAGE (BY BETA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE        672   673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687   688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE        704   704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                               (BY SIMILARITY).
FT   SITE        706   706       INVOLVED IN OXIDATIVE REACTIONS
FT                               (BY SIMILARITY).
FT   SITE        711   712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                               (BY SIMILARITY).
FT   SITE        713   714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                               (BY SIMILARITY).
FT   SITE        720   721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                               (BY SIMILARITY).
FT   SITE        724   734       BASOLATERAL SORTING SIGNAL
FT                               (BY SIMILARITY).
FT   SITE        739   740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                               (BY SIMILARITY).
FT   SITE        757   760       ENDOCYTOSIS SIGNAL.
FT   SITE        759   762       NPXY MOTIF.
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Query Match 98.2%; Score 3585.5; DB 1; Length 770;
Best Local Similarity 90.0%; Pred. No. 1.7e-170;
Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLRKTTREPLTRD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
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Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 3
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      316    344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      363    428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      504    521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      713    732       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND.
FT   SITE        652    653       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        653    654       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        668    669       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        685    685       INVOLVED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        687    687       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        692    693       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        694    695       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        701    702       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                (BY SIMILARITY).
FT   SITE        705    715       BASOLATERAL SORTING SIGNAL
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                (BY SIMILARITY).
FT   SITE        738    741       ENDOCYTOSIS SIGNAL.
FT   SITE        740    743       NPXY MOTIF.
FT   METAL       137    137       COPPER (BY SIMILARITY).

  Query Match             98.0%;  Score 3579;  DB 1;  Length 751;
  Best Local Similarity   91.9%;  Pred. No. 3.4e-170;
  Matches  690;  Conservative    2;  Mismatches    3;  Indels   56;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRDRKQCKTHPHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVEFVCCPLAEESDHVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATITTTTTIESVEEVVR------------ 288
              |||:|||||||||||||||||||||||||||||||||||||||||||||
Db        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATITTTTTIESVEEVVREVCSEQAETGPC 300

Qy        289 ----------------------------------------------VPTTAASTPDAVDKYL 304
                                                           :|||||||||||||||
Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVIPTTAASTPDAVDKYL 360

Qy        305 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 364
              ||||||||||||||||||:|||||||||||||||||:|||||||||||||||:::|||||||
Db        361 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 420

Qy        365 ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR 424
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db        421 ESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVR 480

Qy        425 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQ 540

Qy        485 DEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 DEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 600

Qy        545 PWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDS 660

Qy        605 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVD 664
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        661 GYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 720

Qy        665 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||
Db        721 AAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751


RESULT 4
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
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DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC       nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clatherin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-linked glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
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DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL       1     17       BY SIMILARITY.
FT   CHAIN       18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN       18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN       18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN      672    770       C99 (BY SIMILARITY).
FT   CHAIN      672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN      672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN      688    770       C83 (BY SIMILARITY).
FT   CHAIN      688    713       P3(42) (BY SIMILARITY).
FT   CHAIN      688    711       P3(40) (BY SIMILARITY).
FT   CHAIN      712    770       GAMMA-CTF(59).
FT   CHAIN      714    770       GAMMA-CTF(57).
FT   CHAIN      721    770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN      740    770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN      18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   700    723       POTENTIAL.
FT   DOMAIN     724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     135    155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN     181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN     291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN     391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN     732    751       INTERACTION WITH G(O)-ALPHA (BY
FT                               SIMILARITY).
FT   DOMAIN     230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN     274    280       POLY-THR.
FT   SITE       144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                               (BY SIMILARITY).
FT   ACT_SITE   301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE       671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE       672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE       687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE       704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                               (BY SIMILARITY).
FT   SITE       706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                               (BY SIMILARITY).
FT   SITE       711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                               (BY SIMILARITY).
FT   SITE       713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                               (BY SIMILARITY).

  Query Match             96.6%;  Score 3530.5;  DB 1;  Length 770;
  Best Local Similarity   88.3%;  Pred. No. 8.8e-168;
  Matches  680;  Conservative    8;  Mismatches    7;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||||||:|||||||||||:|||||||||||||||:|||||:|||||:|||:||:|||||||
Db          1 MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||||| ||| |||||| | ||||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||:|||||||||||||||||||:|||||||||||:|||||:|||:||||
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||:|||||||||||||||||||||||||||||||||||||||||||||
Db        241 EAEDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLLKTTQEHLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 5
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
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RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apolipoproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q06495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q06495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clatherin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC       sulfate to the L-APP isoforms produces the APP proteoglycan core
CC       proteins, the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (BY SIMILARITY).

  Query Match             96.3%;  Score 3517.5;  DB 1;  Length 770;
  Best Local Similarity   88.1%;  Pred. No. 3.9e-157;
  Matches  678;  Conservative    7;  Mismatches   10;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||  |:|||||||||||||:||||:|||||.:|||| ||| ||||: |.||||.
Db          1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| :|||||||||||||||||||||||||||||||||||||| |||||||:|||||||||.
Db         61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||.|||||.|||| ||||||||||:||||:|||| |||:|||||| |||:|||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||||:|:|||||||||||:|||||.|||||:|||||.|||||||:|.||
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288
              ||||||| :|||||||||||||||||:|||||'|||||||||||:||
Db        241 EADDDEDVEDGDEVEEEAEEPYEEATFKTTSIATTTTTTTESVEEVVRFVCSEQAETGPC 300

Qy        289 ---------------------------------------------------------- 288

Db        301 RSMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQNLLKTSGEPVSQG 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||| || ||||||||||||:|||||'|||||.||| ||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
              |||:|||||||||||||||||||||||||||||||||||||||||||.|||||||  |||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVIPEERHLSKMQQNGYENPIYKFFEQMQN 770


RESULT 6
A4_MOUSE
ID   A4_MOUSE       STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Kaha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein C.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN [8]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [9]
RP SEQUENCE OF 656-737 FROM N.A.
RC STRAIN=129/Sv;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA Loring J.F., Goate A.M.;
RT "Introduction of six mutations into the mouse genome using 'Hit and
RT Run' gene-targeting: introduction of familial Alzheimer's disease
RT mutations into the mouse amyloid precursor protein gene and
RT humanization of the A-beta fragment.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX PubMed=8510506;
RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT "Regional distribution of the alternatively spliced isoforms of beta
RT APP RNA transcript in the brain of normal, heterozygous and
RT homozygous weaver mutant mice as revealed by in situ hybridization
RT histochemistry.";
RL Brain Res. Mol. Brain Res. 17:340-346(1993).
RN [11]
RP INTERACTION WITH KNS2.
RX PubMed=11144355;
RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT "Axonal transport of amyloid precursor protein is mediated by direct
RT binding to the kinesin light chain subunit of kinesin-I.";
RL Neuron 28:449-459(2000).
RN [12]
RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP THR-743; TYR-757; ASN-759 AND TYR-762.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [13]
RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX MEDLINE=22028091; PubMed=11912189;
RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT with scaffold proteins of the JNK signaling cascade.";
RL J. Biol. Chem. 277:20070-20078(2002).
RN [14]
RP INTERACTION OF CTF PEPTIDES WITH NUMB.
RX PubMed=12011466;
RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT "The gamma-secretase-generated intracellular domain of beta-amyloid
RT precursor protein binds Numb and inhibits Notch signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN [15]
RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX PubMed=11553691;
RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT gamma-secretase is rapidly degraded but distributes partially in a
RT nuclear fraction of neurones in culture.";
RL J. Neurochem. 78:1168-1178(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions. Can promote transcription activation through binding
CC to APBB1/Tip60 and inhibit Notch signaling through interaction
CC with Numb. Couples to apoptosis-inducing pathways such as those
CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
CC similarity). Acts as a kinesin I membrane receptor, mediating the
CC axonal transport of beta-secretase and presenilin 1. May be
CC involved in copper homeostasis/oxidative stress through copper ion
CC reduction. Can regulate neurite outgrowth through binding to
CC components of the extracellular matrix such as heparin and
CC collagen I and IV (By similarity). The splice isoforms that
CC contain the BPTI domain possess protease inhibitor activity (By
CC similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis.
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC its serine phosphorylation. Also interacts with GPCR-like protein
CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC MT-binding domains (By similarity). Associates with microtubules
CC in the presence of ATP and in a kinesin-dependent manner (By
CC similarity). Interacts, through a C-terminal domain, with GNAO1
CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clatherin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 95.5%; Score 3488.5; DB 1; Length 770;
Best Local Similarity 87.7%; Pred. No. 1.1e-165;
Matches 675; Conservative 6; Mismatches 14; Indels 75; Gaps 1;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
||| |||||||||| |||||||||||||||||||||||:|||||||||||:|||||||
Db 1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
||| |||||||||||||||||||||||||||||||||||||||| | |||||||||
Db 61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

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Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              ||||||||||||||:|||||||||||||||||||||||||||| |||||  |||||||:|||
Db        181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||||||| |||||||||||||||||||| ||| ||||||||||||.||
Db        241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTTESVEEVVRFVCSFQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGSVSTQSLLKTTSEPLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 ||||||||||||||||||||||||||||||||||||||||||| |||.|||||.|||
Db        361 PDKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              |||||||||||||||||||||||||||||||||| |||||||||| ||| |||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              |||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||| |
Db        481 QAVPPRPHHVFNMLKKYVRAEQKDRQHILKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
              |||||||||||||||||||| || |||||||.|||||||||||||||||||| ||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
              |||||||||||||| | |||| ||||||||||||||| |||||||| |||| |||
Db        661 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
```

RESULT 7
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA Mytilineou C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX PubMed=8996834;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX PubMed=9930726;
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA Suzuki T., Nairn A.C., Greengard P.;
RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND HIS-733.
RX PubMed=10024358;
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Go heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;

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RA   Liu S.T., Howlett G., Barrow C.J.;
RT   "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT   of the A beta peptide of Alzheimer's disease.";
RL   Biochemistry 38:9373-9378(1999).
RN   [12]
RP   IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP   GLY-704.
RX   PubMed=11959460;
RA   Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT   "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT   peptide 1-42-associated oxidative stress and neurotoxicity.";
RL   Biochim. Biophys. Acta 1586:190-198(2001).
RN   [13]
RP   PHOSPHORYLATION.
RX   PubMed=9085254;
RA   Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA   Greengard P., Suzuki T.;
RT   "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT   phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT   cultured cells.";
RL   Mol. Med. 3:111-123(1997).
RN   [14]
RP   PHOSPHORYLATION ON SER-730.
RX   PubMed=10329382;
RA   Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA   Greengard P., Nairn A.C., Suzuki T.;
RT   "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT   precursor protein at Ser655 by a novel protein kinase.";
RL   Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN   [15]
RP   PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP   THR-743.
RX   MEDLINE=99274744; PubMed=10341243;
RA   Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA   Kirino Y., Greengard P., Suzuki T.;
RT   "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT   during neuronal differentiation.";
RL   J. Neurosci. 19:4421-4427(1999).
RN   [16]
RP   PHOSPHORYLATION ON THR-743.
RX   PubMed=10936190;
RA   Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA   Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT   "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT   protein by cyclin-dependent kinase 5.";
RL   J. Neurochem. 75:1085-1091(2000).
RN   [17]
RP   CARBOHYDRATE STRUCTURE OF APPICAN.
RX   PubMed=11479316;
RA   Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA   Sugahara K., Robakis N.K.;
RT   "Appican, the proteoglycan form of the amyloid precursor protein,
RT   contains chondroitin sulfate E in the repeating disaccharide region
RT   and 4-O-sulfated galactose in the linkage region.";
RL   J. Biol. Chem. 276:37155-37160(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC       G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC       mediating the axonal transport of beta-secretase and presenilin 1
CC       (By similarity). May be involved in copper homeostasis/oxidative
CC       stress through copper ion reduction. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I and IV (By similarity). The
CC       splice isoforms that contain the BPTI domain possess protease
CC       inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain.
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity). Interacts,
CC       through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC       CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC       associates with HADH2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clatherin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the

  Query Match             95.5%;  Score 3488.5;  DB 1;  Length 770;
  Best Local Similarity   87.5%;  Pred. No. 1.1e-165;
  Matches  674;  Conservative    8;  Mismatches   13;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| |||||||||| ||||||||||||||||||||||||:|||||||||||||:|||||||
Db          1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| |||||||||||||||||||||||||||||||||||||||||| 1 |||||||||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||::||||||||||||||||||||||| |||||||||||||:||||
Db        181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||:|||, |||:|||||||||||||||||||||||||||||||||||
Db        241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVSSQSLLKTTSEPLPQD 360

Qy        289 ---VPTIAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                  :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
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                ||||||||||||||||||||| || |||:|||||||:|||||:|||:||||||.|||.|||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
              |||||||||||||||| ||||:|| ||||||||||:|||||.|||||||||||:|||||| |||
Db        661 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||||:|||||||||||||||||:|||||:|||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770


RESULT 8
APP2_MOUSE
ID   APP2_MOUSE     STANDARD;      PRT:   695 AA.
AC   Q06335;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).
GN   APLP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RA   von der Kammer H.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-246 FROM N.A.
RX   MEDLINE=94032480; PubMed=8218408;
RA   Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;
RT   "The complete cDNA coding sequence for the mouse CDEI binding
RT   protein.";
RL   Biochim. Biophys. Acta 1216:154-156(1993).
RN   [3]
RP   SEQUENCE OF 185-695 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Heart;
RX   MEDLINE=93129193; PubMed=1482349;
RA   Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
RT   "A murine sequence-specific DNA binding protein shows extensive local
RT   similarities to the amyloid precursor protein.";
RL   Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
RN   [4]
RP   SEQUENCE OF 1-35 FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=96029629; PubMed=7592716;
RA   von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
RA   Gilbert D.J., Jenkins N.A., Sisodia S.S.;
RT   "The mouse APLP2 gene. Chromosomal localization and promoter
RT   characterization.";
RL   J. Biol. Chem. 270:25475-25480(1995).
CC   -!- FUNCTION: BINDS TO THE DNA 5'-GTCACATG-3'(CDEI BOX) WHICH PLAYS
CC       AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC       (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z22592; CAA80306.1; -.
DR   EMBL; M97216; AAA20039.1; -.
DR   EMBL; U34291; AAC52318.1; -.
DR   PIR; S38344; S38344.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88047; Aplp2.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Transmembrane; DNA-binding; Signal; Nuclear protein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    695       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    624       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    625    648       POTENTIAL.
FT   DOMAIN      649    695       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    294       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      218    231       POLY-GLU.
FT   DOMAIN      256    266       POLY-GLU.
FT   CARBOHYD    485    485       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    185    189       GMLLP -> MACCC (IN REF. 3).
SQ   SEQUENCE   695 AA;  78944 MW;  BBF4B95AAB2A0311 CRC64;

  Query Match           47.4%;  Score 1730;  DB 1;  Length 695;
  Best Local Similarity 49.2%;  Pred. No. 9.6e-79;
  Matches  359;  Conservative  118;  Mismatches  163;  Indels   90;  Gaps   19;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | :|||   :| | :          |||    :|||||||:|:|||||:|:| |||: ||
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :||||:|: ||| :|:|||||:|||||||||:|||||| | :||:| ::|||:  | ||'::
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||||||||| |||:| |:| |||||:||| |  |||: |: |  :   |: ||||||||:
Db        133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLIEGLTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAE---E 231
              :|  | |:|||  :  :|||:  | : ||::          |  |  ||  :: :|   |
Db        193 DQFHGTEYVCCPQTKTVDSDSTMSKEEEEEEE---------DEEDEEEDYDLDKSEFPTE 243

Qy        232 EEVAEVEEEEAD-DDEDDEDGDEVEEEAE--------EPYEEATERTTSIATTTTTTIES 282
              :: :  |  || ::|||:|:|:|| |: :        : | |  |  |  ::  | : :
Db        244 ADLEDFTEAAADEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTISDKE 301

Qy        283 VEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAE 342
              :  |:|| |   | | || |||  |:|||| ||||||:|| :|| || :| :||||||
Db        302 IVHDVKVPPTPLPTND-VDVYLETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAE 360

Qy        343 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYI 402
              |||||| ::: :|||||  |::||:|||:|:|||||||:|||||||||||||:|||||:
Db        361 LQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYL 420

Qy        403 TALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 462
              |||: |||| :   |::|||||| ||| ||:::|::|| |||:||||::|||||| ||
Db        421 AALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVI 480

Qy        463 YERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSL 522
              || ||||:||| || ||:|||:|:||||||::       |:|          |    |:
Db        481 EERRNQSLTLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSSI 523

Qy        523 TETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSG 582
              :|    | :    | :    | | |     |: :|||           |:  : | |
Db        524 SENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----------GSGMAEQDG-G 566

Qy        583 LTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NK 624
              |   : : | |: |||      |   :|  ::::| || ||                 :
Db        567 LIGAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPESVGPLREDFSLSS 624

Qy        625 GAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYEN 684
              |:|||:|  | ||||| |:|||:|:|| :| ||:|||  :|||||||:||| :||||
Db        625 NALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYEN 684

Qy        685 PTYKFFEQMQ 694
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                    ||||: ||||
Db          685 PTYKYLEQMQ 694


RESULT 9
APP2_HUMAN
ID   APP2_HUMAN     STANDARD;      PRT;   763 AA.
AC   Q06481;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE   (CDEI-box binding protein) (CDEBP).
GN   APLP2 OR APPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=93250009; PubMed=8485127;
RA   Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA   Norris K., Foster D.C.;
RT   "Molecular cloning of the cDNA for a human amyloid precursor protein
RT   homolog: evidence for a multigene family.";
RL   Biochemistry 32:4481-4486(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=95217334; PubMed=7702756;
RA   von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
RT   "A human amyloid precursor-like protein is highly homologous to a
RT   mouse sequence-specific DNA-binding protein.";
RL   DNA Cell Biol. 13:1137-1143(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94035131; PubMed=8220435;
RA   Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA   Hyman B.T., Neve R.L., Tanzi R.E.;
RT   "Isolation and characterization of APLP2 encoding a homologue of the
RT   Alzheimer's associated amyloid beta protein precursor.";
RL   Nat. Genet. 5:95-99(1993).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Lung;
RX   MEDLINE=22386257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC       SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC       FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC       MAY BIND TO THE DNA 5'-GTCACATG-3'(CDEI BOX).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC       (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=Q06481-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q06481-2; Sequence=VSP_000018;
CC       Name=3;
CC         IsoId=Q06481-3; Sequence=VSP_000019;
CC   -!- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
CC       AND ENDOTHELIAL TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S60099; AAC60589.1; -.
DR   EMBL; L09209; AAA35526.1; -.
DR   EMBL; Z22572; CAA80295.1; -.
DR   EMBL; L27631; AAC41701.1; -.
DR   EMBL; BC000373; AAH00373.1; -.
DR   PIR; A49321; A49321.
DR   HSSP; P05067; 1MWP.
DR   GeneW; HGNC:598; APLP2.
DR   MIM; 104776; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0003677; F:DNA binding activity; NAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Signal; Alternative splicing; DNA-binding;
KW   Nuclear protein; Serine protease inhibitor.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    763       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    692       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    693    716       POTENTIAL.
FT   DOMAIN      717    763       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      215    280       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      306    364       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      215    231       POLY-GLU.
FT   ACT_SITE    320    321       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    310    360       BY SIMILARITY.
FT   DISULFID    319    343       BY SIMILARITY.
FT   DISULFID    335    356       BY SIMILARITY.
FT   VARSPLIC    308    363       Missing (in isoform 2).
FT                                /FTId=VSP_000018.
FT   VARSPLIC    613    624       Missing (in isoform 3).
FT                                /FTId=VSP_000019.
FT   CONFLICT    543    543       S -> I (IN REF. 1).
SQ   SEQUENCE   763 AA;  86955 MW;  CA3A7D6DDB8A28D0 CRC64;

  Query Match             47.2%;  Score 1723;  DB 1;  Length 763;
  Best Local Similarity   47.0%;  Pred. No. 2.4e-78;
  Matches  371;  Conservative  112;  Mismatches  166;  Indels  140;  Gaps   20;
```

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Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
Db         15 LLLLLLVGLTAPALALAGYIEALAANAGTGPAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
Db         75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
Db        133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
Db        193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-------EEEEEDEEEDYDVYKSEFPTEAD 245

Qy        237 VEE--EEA--DDDEDDEDGDEVEEEAEEPY----------EEATERTTSIATTTTTTTES 282
Db        246 LEDFTEAAVDEDDEDEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy        283 VEEV-------------------------------------------------------VRVP 298
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMIP 365

Qy        299 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPK 358
Db        366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy        359 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPP 418
Db        425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPP 484

Qy        419 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 478
Db        485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIYERRNQSL 544

Qy        479 SLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLIETKTTVE 538
Db        545 SLLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTASISETPVDVR 587

Qy        539 LLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN----- 593
Db        588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGGL 635

Qy        594 IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS---------  -----NKG 639
Db        636 IGAEEKVINSKNKVDENMVIDEILDV--KEMIFNAERVGGLEEERESVGPLREDFSLSSS 693

Qy        640 AIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENP 699
Db        694 ALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENP 753

Qy        700 TYKFFEQMQ 708
Db        754 TYKYLEQMQ 762
```

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RESULT 10
APP2_RAT
ID   APP2_RAT       STANDARD;      PRT;   765 AA.
AC   P15943;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
GN   APLP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-627 FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain, and Heart;
RX   MEDLINE=94368849; PubMed=8086458;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT   protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT   difference to human and murine homologues.";
RL   Biochim. Biophys. Acta 1219:167-170(1994).
RN   [2]
RP   SEQUENCE OF 575-765 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=90207205; PubMed=1690887;
RA   Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT   "Characterization of cDNA encoding a human sperm membrane protein
RT   related to A4 amyloid protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=P15943-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=P15943-2; Sequence=VSP_000021;
CC       Name=C;
CC         IsoId=P15943-3; Sequence=VSP_000020;
CC       Name=D;
CC         IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X77934; CAA54906.1; -.
DR   EMBL; M31322; AAA42352.1; -.
DR   PIR; A35981; A35981.
DR   PIR; S42880; S42880.
DR   HSSP; P05067; 1MWP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Alternative splicing; Serine protease inhibitor;
KW   Signal; Glycoprotein.
FT   SIGNAL       1     29       POTENTIAL.
FT   CHAIN       30    765       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN      30    695       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   696    718       POTENTIAL.
FT   DOMAIN     719    765       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     218    282       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN     308    366       BPTI/KUNITZ INHIBITOR.
FT   ACT_SITE   322    323       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID   312    362       BY SIMILARITY.
FT   DISULFID   321    345       BY SIMILARITY.
FT   DISULFID   337    358       BY SIMILARITY.
FT   DOMAIN     218    229       POLY-GLU.
FT   CARBOHYD   628    628       O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT   VARSPLIC   311    365       Missing (in isoform C and isoform D).
FT                               /FTId=VSP_000020.
FT   VARSPLIC   616    627       Missing (in isoform B and isoform D).
```

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FT                              /FTId=VSP_000021.
FT   CONFLICT    575    577       DQF -> EFV (IN REF. 2).
SQ   SEQUENCE   765 AA;  86882 MW;  CF51FCCCE305A0CF CRC64;

  Query Match             46.8%;  Score 1711;  DB 1;  Length 765;
  Best Local Similarity   46.1%;  Pred. No. 9.4e-78;
  Matches  363;  Conservative  122;  Mismatches  167;  Indels  136;  Gaps   20;

Qy          5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | :|||   || |  :         :||    :||||:|||| :|||||: :| |||: |:
Db         15 LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPDP 74

Qy         57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              :|||:|: ||| :|||||:|:|||||||||| | :|:|:| :||.::  | ||||:
Db         75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

Qy        117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
              |||||||||| |||| |:| |||||:||| | |||| || |  :   |: ||:|||||:
Db        133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMILYSYGMLLPCGV 192

Qy        177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDDSDVWWGGADTDYA-DGSEDKVVEVAEEEE 233
              |:| | |:|||| :  :|||:  | : ,|:: :      :  || | :|       |:
Db        193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEE----DEEEDYALDKSEFPTEADLEDFT 248

Qy        234 VAEVEEEEADDDEDDEDGDEVEEEAEEPYEE------ATERTTSIATTTTTTTTESVEEVV 287
              |  :|:| :::|::|:|:|| |: :  |:         | | ::  | : : :   |
Db        249 EAAADEDEDEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKEIAHDV 308

Qy        288 R----------------------------------------------------------VPT 291
              :                                                           :|
Db        309 KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMIPP 368

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
              |   | | || | :|  .:|||| ||||||:|| :|| *| :| :|||||| |||| |||
Db        369 TPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRSRMDRVKKEWEEAELQAKNLPKA 427

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPR 411
              ::: :|||||  |::||:|||:|:|||||||:|||||||||||:|||||: ||||: |||
Db        428 ERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRIALENYLAALQSDPPR 487

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
              |  :   |::|||| | : ||::|::||  |||:|| |::|:|||| :| || :||||
Db        488 PHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQSLS 547

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
              ||: || |::|||:|:| |||:::      |:|         |   .::|   |
Db        548 LLYKVPYVAQEIQEEIDELLQEQR-------ADM----------DQFTSSISENPVDVR- 589

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTN-----I 586
              ,: | | ::: |:| |      ': :|||    | ::     :  : :||:         |
Db        590 --VSSEES-EEIPPFHPF--HPFPSLSENE----DIQPELYHPM--KKGSGMAEQDGGLI 638

Qy        587 KTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS----------------NKGA 626
                ||    ': |||     |   :|  ::::| || ||                    :
Db        639 GAEEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEPDSVGPLREDFSLSSSA 696

Qy        627 IIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPT 686
              :|||:|  | |||| |:||||:|:|| :| ||:|'|   :'||||':||| :|||| |
Db        697 LIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPMLTPEERHLNKMQNHGYENPT 756

Qy        687 YKFFEQMQ 694
              ||: ||||
Db        757 YKYLEQMQ 764


RESULT 11
APP1_HUMAN
ID   APP1_HUMAN     STANDARD;      PRT;   650 AA.
AC   P51693; O00113; Q96A92;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN   APLP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98088960; PubMed=9428684;
RA   Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L., Multhaup G.,
RA   Masters C.L., Beyreuther K., Weidemann A.;
RT   "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
RT   expression in COS-7 cells and identification of soluble forms in the
RT   cerebrospinal fluid.";
RL   Eur. J. Biochem. 250:354-363(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98180887; PubMed=9521588;
RA   Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
RA   Olsen A., Tryggvason K.;
RT   "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT   19q13.1.";
RL   Hum. Genet. 102:192-196(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
RX   MEDLINE=96115107; PubMed=7494461;
RA   Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
RA   Black I.B.;
RT   "Selective localization of amyloid precursor-like protein 1 in the
RT   cerebral cortex postsynaptic density.";
RL   Brain Res. Mol. Brain Res. 32:36-44(1995).
RN   [5]
RP   HEPARIN AND ZINC BINDING.
RX   MEDLINE=95014513; PubMed=7929392;
RA   Bush A.I., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RT   "The amyloid beta-protein precursor and its mammalian homologues.
RT   Evidence for a zinc-modulated heparin-binding superfamily.";
RL   J. Biol. Chem. 269:26618-26621(1994).
RN   [6]
RP   INTERACTION WITH APBA2.
RX   MEDLINE=99107877; PubMed=9890987;
RA   Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA   Sakiyama S., Kirino Y., Suzuki T.;
RT   "Interaction of a neuron-specific protein containing PDZ domains with
RT   Alzheimer's amyloid precursor protein.";
RL   J. Biol. Chem. 274:2243-2254(1999).
RN   [7]
RP   EXTRACELLULAR COPPER-BINDING.
RX   MEDLINE=22130992; PubMed=12135352;
RA   Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,
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RA   Reed J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
RA   Bayer T.A., Multhaup G.;
RT   "Evidence for a copper-binding superfamily of the amyloid precursor
RT   protein.";
RL   Biochemistry 41:9310-9320(2000).
CC   -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC       gamma-secretase processed fragment, AL1D1, activates transcription
CC       activation through APBB1 (Fe65) binding (By similarity). Couples
CC       to JIP signal transduction through C-terminal binding. May
CC       interact with cellular G-protein signaling pathways. Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I.
CC   -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC       neuronal apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB and APBA family members,
CC       MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC       serine phosphorylation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC       processed in the Golgi complex.
CC   -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
CC       localized to the postsynaptic density (PSD).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The NPXY site is also involved in clatherin-mediated
CC       endocytosis.
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal
CC       apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
CC       similarity).
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: O-glycosylated.
CC   -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC       Zinc-binding increases heparin binding. No Cu(II) reducing
CC       activity with copper-binding.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U48437; AAB96331.1; -.
DR   EMBL; AD000864; AAB50173.1; -.
DR   EMBL; BC012889; AAH12889.1; -.
DR   HSSP; P05067; 1MWP.
DR   Genew; HGNC:597; APLP1.
DR   MIM; 104775; -.
DR   GO; GO:0005604; C:basement membrane; TAS.
DR   GO; GO:0005208; F:amyloid protein; TAS.
DR   GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR   GO; GO:0007399; P:neurogenesis; TAS.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW   Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW   Glycoprotein.
FT   SIGNAL       1     38       POTENTIAL.
FT   CHAIN       39    650       AMYLOID-LIKE PROTEIN 1.
FT   CHAIN      621    650       C30 (BY SIMILARITY).
FT   DOMAIN      39    580       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   581    603       POTENTIAL.
FT   DOMAIN     604    650       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     158    178       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN     204    211       ZINC-BINDING.
FT   DOMAIN     310    342       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     410    441       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     442    459       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN     640    643       CLATHRIN-BINDING (POTENTIAL).
FT   DOMAIN     241    247       POLY-GLU.
FT   DOMAIN     264    268       POLY-GLU.
FT   SITE       167    167       REQUIRED FOR COPPER(II) REDUCTION (BY
FT                               SIMILARITY).
FT   SITE       604    615       BASOLATERAL SORTING SIGNAL (BY
FT                               SIMILARITY).
FT   SITE       620    621       CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT   SITE       638    641       ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT   SITE       640    643       NPXY MOTIF.
FT   CARBOHYD   337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   461    461       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   551    551       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    48     48       A -> P (IN REF. 1).
SQ   SEQUENCE   650 AA;  72176 MW;  B95F0F4D1C5CBAC7 CRC64;

  Query Match           32.4%;  Score 1185;  DB 1;  Length 650;
  Best Local Similarity  38.7%;  Pred. No. 8.2e-52;
  Matches  271;  Conservative  115;  Mismatches  231;  Indels   84;  Gaps   16;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              :|| | ||| |     :|   : | |      |:| |||| :| ::: |:|: |:  ::
Db         23 LLPLLLLLLRAQPAIGSLAGGSPGAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRSR 82

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCLV 119
               :   : :|:|:::|||||  | :| | : :: ||   |     ||| |:|:|||
Db         83 RCLRDPQRVLEYCRQMYPELQIARVEQATQAIPMERWCGGSRSGSCAHPHHQVVPFRCLP 142

Qy        120 GEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKF 179
              '||||:|||||: |:|||||||| ||:    |  |:| || :  .|  |||||| |:|
Db        143 GEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDRF 202

Qy        180 RGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEE 239
              ||||:|||'     |  |  | | |  |          ||    ||  ||:||    ||
Db        203 RGVEYVCCPPPGTPD--PSGTAVGDPSTRSW-------PPGSR---VEGAEDEE----EE 246

Qy        240 EEADDDEDD--EDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
              |      :|   :  ||| ||      :  | ::    | |           ||
Db        247 ESFPQPVDDYFVEPPQAEEE-EETVPPPSSHTLAVVGKVTPTPR--------PT------ 291

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              | || |   ||: :||  | :||  || :   ::::|||||  |: |:||| ||||::|:
Db        292 DGVDIYFGMPGEISEHEGFLRAKMDLEERRMRQINEVMREWAMADNQSKNLPKADRQALN 351

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              :|||  :::||:: : |||:||||,|  || |::||:|| ||| :: |||| ||:   |
Db        352 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQADPPQAERVLL 411

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
               |::|:||||,:::|||:|::||  |||:|| |:| || ||||:|| ||:|||| ||   |
Db        412 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVHTHLQVIEERVNQSLGLLDQNP 471

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE 537
              :|:|:: :: ||| |                    | || |       | |
Db        472 HLAQELRPQIQELLHSEH--------------------LGPSELEA-------PAPGG 502

Qy        538 FSLD--DLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVK 595
              | |   ||| |  | |                    :| | :  :     |   : : :
Db        503 SSEDKGGLQPPDS--KDDTPM-------------TLPKGSTEQDAASPEKEKMNPLEQYE 547

Qy        596 MDAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVML-KKK 651
                      |:  |    |:        | :: |: ||:: |    ::| :::::| :||
Db        548 RKVNASVPRGFPFHSSEIQRDELAPAGTGVSREAVSGLLIMGAGGGSLIVLSMLLLRRKK 607

Qy        652 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
              | :| |||||||  :| ||: | ::|::|||||||:| |:
Db        608 PYGAISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 648


RESULT 12
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APP1_MOUSE
ID   APP1_MOUSE     STANDARD;      PRT:   653 AA.
AC   Q03157; Q8VC38;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN   APLP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=93066322; PubMed=1279693;
RA   Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
RA   Solomon F.;
RT   "Identification of a mouse brain cDNA that encodes a protein related
RT   to the Alzheimer disease-associated amyloid beta protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   COLLAGEN-BINDING.
RX   MEDLINE=96139497; PubMed=8576160;
RA   Beher D., Hesse L., Masters C.L., Multhaup G.;
RT   "Regulation of amyloid protein precursor (APP) binding to collagen and
RT   mapping of the binding sites on APP and collagen type I.";
RL   J. Biol. Chem. 271:1613-1620(1996).
RN   [4]
RP   INTERACTION WITH DAB1.
RX   MEDLINE=99389880; PubMed=10460257;
RA   Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT   "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RT   protein 1.";
RL   J. Neurosci. 19:7507-7515(1999).
RN   [5]
RP   INTERACTION WITH MAPK8IP1.
RX   MEDLINE=21408156; PubMed=11517249;
RA   Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA   Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA   Kyriakis J.M., Nishimoto I.;
RT   "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT   scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL   J. Neurosci. 21:6597-6607(2001).
RN   [6]
RP   GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
RP   TYR-641.
RX   MEDLINE=22313598; PubMed=12228233;
RA   Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
RT   "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RT   secretase regulates transcription.";
RL   J. Biol. Chem. 277:44195-44201(2002).
CC   -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC       gamma-secretase processed fragment, ALID1, activates transcription
CC       activation through APBB1 (Fe65) binding. Couples to JIP signal
CC       transduction through C-terminal binding. May interact with
CC       cellular G-protein signaling pathways. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I.
CC   -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC       neuronal apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB and APBA family members,
CC       MAPK8IP1 and Dabl (By similarity). Binding to Dabl inhibits its
CC       serine phosphorylation.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC       processed in the Golgi complex.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The NPXY site is also involved in clatherin-mediated
CC       endocytosis.
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal
CC       apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC       similarity).
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: O-glycosylated.
CC   -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC       Zinc-binding increases heparin binding. No Cu(II) reducing
CC       activity with copper-binding.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L04538; AAA37247.1; -.
DR   EMBL; BC021877; AAH21877.1; -.
DR   PIR; A46362; A46362.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88046; Aplp1.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW   Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW   Glycoprotein.
FT   SIGNAL        1     37       POTENTIAL.
FT   CHAIN        38    653       AMYLOID-LIKE PROTEIN 1.
FT   CHAIN       624    653       C30 (BY SIMILARITY).
FT   DOMAIN       38    583       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    584    606       POTENTIAL.
FT   DOMAIN      607    653       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      157    177       COPPER-BINDING.
FT   DOMAIN      203    210       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      313    345       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      413    444       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      445    462       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      263    271       POLY-GLU.
FT   DOMAIN      535    538       POLY-SER.
FT   DOMAIN      601    606       POLY-LEU.
FT   SITE        166    166       REQUIRED FOR COPPER(II) REDUCTION (BY
FT                                SIMILARITY).
FT   SITE        607    618       BASOLATERAL SORTING SIGNAL (BY
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FT                                   SIMILARITY).
FT   SITE         623    624         CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT   SITE         641    644         ENDOCYTOSIS SIGNAL.
FT   SITE         643    646         NPXY MOTIF.
FT   CARBOHYD     464    464         N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     554    554         N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MUTAGEN      641    641         Y->G: REDUCED BINDING OF APBB1.
FT   CONFLICT      17     17         P -> PP (IN REF. 2).
SQ   SEQUENCE   653 AA;  72750 MW;  56516DC3EA40E4BC CRC64;

  Query Match             32.3%;  Score 1180;  DB 1;  Length 653;
  Best Local Similarity   38.4%;  Pred. No. 1.5e-51;
  Matches  269;  Conservative  121;  Mismatches  232;  Indels   78;  Gaps   17;

Qy          1 MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGT 59
              :|| |:|:|| |  |    | | :     .        |:|  :|||  :  ::: |:|: |  :
Db         22 LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLTLHRDLRTGRWEPDPQRS 80

Qy         60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
              : |:   : :|::|:::'|:| |  | :|' : :: |:     |      :|  |::: |
Db         81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAIPMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy        119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
               |||||:||||:: |:|:||||||' ||:    |   |:| || :    ||  ||||:|| |:
Db        141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGSDR 200

Qy        179 FRGVEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
              ||||:|||'    :  |       |   :   :   |    ||     |:| ||          :·||
Db        201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-------EEEVESF 248

Qy        238 EEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTP 297
              :    |          :|  || ||       :    |   :   :   :                '|
Db        249 PQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPR--------PT------ 294

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              : || |     ||:  ||   ' :||  ||  :     ::::|:|||  |: |: ||||:|::|:
Db        295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              :|||   :::|:::  :  |.|:||||| ||  |::||:|| ||,  :: |:|   :|:     .
Db        355 EHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
               |::|:|||||:::|:|:|:::||  |:|:|:|:|:||  ||  |::||:||  |:|:|||:|  ||  |
Db        415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVIEERMNQSLGLLDQNP 474

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
               :|:|::  :: |||             ||  :       |  '  :|  |  :|  |
Db        475 HLAQELRPQIQELL----------LAEHLGPSEL----DASVPGSSSEDK---------- 510

Qy        537 EFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
                   |||                 |:: :,     |    :| |  :    |        |     :  :
Db        511 ----GSLQP-------------PESKDDPPVTLP---KGSTDQESSSSGREKLTPLECYEQ 551

Qy        597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVML-KKKQ 652
                         ::  |     |:          | :: |: ||::         ::|  ::.::| |||
Db        552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSLIVLSLLLLRKKKP 611

Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
               |  :|  ||||:||  :| ||:  |  :::|::|||||·|:|  |:
Db        612 YGTISHGVVEVDPMLTLEEQQLRELQRHGYENPTYRFLEE 651

RESULT 13
A4_CAEEL
ID   A4_CAEEL       STANDARD;      PRT;   686 AA.
AC   Q10651; Q18583; Q95ZX1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-amyloid-like protein precursor.
GN   APL-1 OR C42D8.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE OF 6-686 FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=94089766; PubMed=8265668;
RA   Daigle I., Li C.;
RT   "apl-1, a Caenorhabditis elegans gene encoding a protein related to
RT   the human beta-amyloid protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:12045-12049(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Hallsworth K.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   REVISIONS, AND ALTERNATIVE SPLICING.
RA   Waterston R.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=a;
CC         IsoId=Q10651-1; Sequence=Displayed;
CC       Name=b;
CC         IsoId=Q10651-2; Sequence=VSP_000017;
CC         Note=No experimental confirmation available;
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; U00240; AAC46470.1; ALT_INIT.
DR   EMBL; U56966; AAA98722.1; -.
DR   EMBL; U56966; AAK68242.1; -.
DR   PIR; T15795; T15795.
DR   HSSP; P05067; 1MWP.
DR   WormPep; C42D8.8a; CE04209.
DR   WormPep; C42D8.8b; CE27845.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
KW   Signal; Transmembrane; Amyloid; Neurogenesis; Glycoprotein;
KW   Alternative splicing.
FT   SIGNAL         1     21       POTENTIAL.
FT   CHAIN         22    686       BETA-AMYLOID-LIKE PROTEIN.
FT   DOMAIN        22    621       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     622    642       POTENTIAL.
FT   DOMAIN       643    686       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       205    228       ASP-RICH.
FT   DOMAIN       676    679       CLATHRIN-BINDING (POTENTIAL).
FT   CARBOHYD      84     84       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     249    249       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     538    539       Missing (in isoform b).
FT                                 /FTId=VSP_000017.
SQ   SEQUENCE   686 AA;  79434 MW;  A0816858FDD48608 CRC64;

  Query Match             22.4%;  Score 816.5;  DB 1;  Length 686;
  Best Local Similarity   29.1%;  Pred. No. 1.5e-33;
  Matches  222;  Conservative  110;  Mismatches  275;  Indels  155;  Gaps   22;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
                :: || : :| | |  |   |           | :| || | :| : | | :|
```

```
Db          6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKIDDERYA 63

Qy         61 TCIDTKEGILQYCQEVYPELQIINVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||    |  ||:||:: || : |||:|| :  |:| :||:     ||   | | ,  |: |
Db         64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSIN------LHDYGMLLPC 174
              |: |:|| :|  |:| |    | |  : ||   | : | |  : :       : : :|
Db        123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy        175 GIDKFRGVEEVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV 234
              :| | ||||:|||    :|  :  | ::
Db        183 ALDMFTGVEFVCCP----NDQTNKTDVQKIK---------------------------- 209

Qy        235 AEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAA 294
                 |:|: ||||||   :|  ||::|  :|
Db        210 ---EDEDDDDDEDDAYEDDYSEESDEKDEE---------------------------- 236

Qy        295 STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA-----ERQAKNLP 349
              | : | |  :    |||  |:||: |:: |||::: :||:|| :      |:::||:
Db        237 -EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHRKKVDKVMKEWGDLETRYNEQKAKD-P 294

Qy        350 KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL- 405
              |  :|   |    ||: | |||:|    |:::   |  ||::|||:::| |  :|  ||
Db        295 KGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNEKKRDATHDYRQALA 354

Qy        406 -QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE 464
               |    |   || |:|||:||| ||| : :|   | |:||  :  |:  || |
Db        355 THVNKPNKHSVLQSLKAYIRAEEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL 414

Qy        465 RMNQSLSLLYNVP---------AVA--EEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
              |:| :|:|| : |          ||   :: :|||   :  |    |  |  :| :   |
Db        415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE----DSELTPIIHDDEFSK 470

Qy        514 GN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANT---ENEVEP 564
                  |   |: '    :      ::||     | ::   ::    |      |   : :|:
Db        471 NAKLDVKAPTTTAKPVKETDNAKVLPTEASDSEEEADEYYEDEDDEQVKKTPDMKKKVKV 530

Qy        565 VDARP--------------------AADRGLTTRPGSGLTNIKTEE-----TSEVKMDA 598
              || :|                     |          |  |: :::'     | |::::|
Db        531 VDIKPKEIKVTIEEEKKAPKILVETSVQTDDEDDDEDSSSSTSSESDEDEDKNIKELRVDI 590

Qy        599 E---------FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLK 649
              |          :|||        |||:   |   |          ::    :  | |  .    :
Db        591 EPIIDEPASFYRHD--------KLIQSPEVERSASSVFQPYVLASAMFITAICIIAFAIT 642

Qy        650 KKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
                :      | :|||   ||||||:: || ||||:||| ||:
Db        643 NARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFFD 683


RESULT 14
A4_DROME
ID   A4_DROME        STANDARD;       PRT;   887 AA.
AC   P14599; Q9TVV0; Q9U4H3; Q9W5F1;
DT   01-APR-1990 (Rel. 14, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-amyloid-like protein precursor.
GN   APPL OR VND OR BCDNA:GH04413 OR EG:65F1.5 OR CG7727.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89184650; PubMed=2494667;
RA   Rosen D.R., Martin-Morris L., Luo L., White K.;
RT   "A Drosophila gene encoding a protein resembling the human
RT   beta-amyloid protein precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [3]
RP   REVISIONS.
RC   STRAIN=Berkeley;
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Oregon-R;
RX   MEDLINE=20196011; PubMed=10731137;
RA   Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA   Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA   Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA   Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA   Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA   Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
RA   Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
RA   Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA   McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA   Glover D.M.;
RT   "From sequence to chromosome: the tip of the X chromosome of D.
RT   melanogaster.";
RL   Science 287:2220-2222(2000).
RN   [5]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley; TISSUE=Ovary;
RX   MEDLINE=20196012; PubMed=10731138;
RA   Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
RA   Stapleton M., Harvey D.A.;
RT   "A Drosophila complementary DNA resource.";
RL   Science 287:2222-2224(2000).
RN   [6]
RP   SEQUENCE OF 1-83 FROM N.A.
RX   MEDLINE=91184006; PubMed=2127912;
RA   Martin-Morris L.E., White K.;
RT   "The Drosophila transcript encoded by the beta-amyloid protein
RT   precursor-like gene is restricted to the nervous system.";
RL   Development 110:185-195(1990).
CC   -!- FUNCTION: Probably corresponds to the protein encoded by the
CC       essential locus vnd, a gene required for embryonic nervous system
CC       development.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in post-mitotic neurons in the
CC       central and peripheral nervous systems. Within the nervous system
CC       transcripts are not observed in neuroblasts, newly generated
CC       neurons and at least one class of presumed glial cells.
CC   -!- DEVELOPMENTAL STAGE: Expressed in all developmental stages.
CC   -!- DOMAIN: The clathrin-binding site is essential for its association
CC       with x11-alpha, -beta, and -gamma. The sequence specific
CC       recognition extends to peptide residues that are C-terminal to the
CC       NPXY motif. This interaction appears to be independent of
CC       phosphorylation (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J04516; AAA28874.1; -.
DR   EMBL; AE003418; AAF45520.2; -.
DR   EMBL; AL031883; CAA21409.1; -.
DR   EMBL; AL022139; CAA21409.1; JOINED.
DR   EMBL; AL022139; CAA18093.1; -.
DR   EMBL; AL031883; CAA18093.1; JOINED.
DR   EMBL; AF181628; AAD55414.1; -.
DR   EMBL; X55774; CAA39294.1; -.
DR   EMBL; X55775; CAA39294.1; JOINED.
DR   PIR; A32758; A32758.
DR   HSSP; P05067; 1MWP.
DR   FlyBase; FBgn0000108; Appl.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal; Transmembrane; Amyloid; Neurogenesis.
FT   SIGNAL       1     27       POTENTIAL.
FT   CHAIN       28    887       BETA-AMYLOID-LIKE PROTEIN.
FT   DOMAIN      28    813       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   814    834       POTENTIAL.
FT   DOMAIN     835    887       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     877    880       CLATHRIN-BINDING (POTENTIAL).
FT   CARBOHYD   150    150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   237    237       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   240    240       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   574    574       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   177    177       S -> T (IN REF. 1).
FT   CONFLICT   229    229       MISSING (IN REF. 1).
FT   CONFLICT   332    332       V -> M (IN REF. 4).
FT   CONFLICT   743    743       S -> T (IN REF. 1).

SQ   SEQUENCE   887 AA;  98332 MW;  F0F0855AD65A5275 CRC64;

  Query Match            20.7%;  Score 755.5;  DB 1;  Length 887;
  Best Local Similarity  25.6%;  Pred. No. 2.1e-30;
  Matches  234;  Conservative  128;  Mismatches  286;  Indels  265;  Gaps   29;

Qy          7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDSDPSG 58
              ||| : |   ||     | | : |     ||:||: |  |::     : : |:| :| |
Db          9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVTDLSK 63

Qy         59 T---KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
                ||:  |  :| ||:: ||   |||:||::    |  ||:::|     :||    ::
Db         64 KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWI 123

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
              |:||| | | |||||||: | | |       |   : |:       | |:   :  : |||
Db        124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRSFAMLL 182

Qy        173 PCGIDKFRGVEFVCCP------------------------------LAEESDNVD---S 198
              |.||  | ||||||||                              : :| |: |   |
Db        183 PCGISVFSGVEFVCCPKHFKTDETHVKKTDLPVMPAAQINSANDELVMNDEDDSNDSNYS 242

Qy        199 ADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV----------------------AE 236
              || ||: |      | |  | :::   ||:|                           ||
Db        243 KDANEDDLD------DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINAE 296

Qy        237 VEE-EEADDDEDDEDGDEVEEEAEEPY--------------------------EEATER 268
              :  || |: |:|  | | | | |  :                          |:|  :
Db        297 YDSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLKSDSSSPSSAPVAPAPEKAPVK 356

Qy        269 TTSIATTTTTTTESVEEVV----------RVPTTAASTPDAVDKYLETPGDENEHAHFQ 317
              : |: :|   :  :   |              |:|| |    | |         || ::
Db        357 SESVTSTPQLSASAAAFVAANSGNSGTGAGAPPSTAQPTS---DPYFTHFDPHYEHQSYK 413

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKA-------VIQHFQEKVESLEQE 370
              :::||| |||:::::|::| : | : :::  || ||       :   ||  |::||:!
Db        414 VSQKRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFKQRMTARFQTSVQALEEE 473

Qy        371 AANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDR 430
              |: ||   |  || | :| |:| |:  |  ||   ||   ||   ,:| :|| |||
Db        474 GNAEKHQLAAMHQQRVLAHINQRKREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDR 533

Qy        431 QHTLKHFEH-VRMVDP---KKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI--- 483
              | | |: | :    |   : || | : :  | |   :|||:::|   | :: :|
Db        534 AHALAHYRHLLNSGGPGGLEAAASERPRTLERLIDIDRAVNQSMTMLKRYPELSAKIAQL 593

Qy        484 ----------QDEV-------------------------------------------- 487
                       :|::
Db        594 MNDYILALRSKDDIPGSSLGMSEEAEAGILDKYRVEIERKVAEKERLRLAEKQRKEQRAA 653

Qy        488 ------DELLQKEQNYSDDVLANMISE----------------------PRISYGNDAL 518
                   :| |: |    ||:| : ::|                        |    | ||
Db        654 EREKLREEKLRLEAKKVDDMLKSQVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAA 713

Qy        519 M-----PSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADR 573
              :     |:|  ||:          |  | | :   :|  :| :      | |      | |
Db        714 LVTAANPNLETTKS---------EKDLSDTE----YGEATVSSTKVQTVLPTVDDDAVQR 760

Qy        574 GLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---G 625
              :     :          ::  : : : :|   ::: |::  |     ||:    : |
Db        761 AVEDVAAA---------VAHQEAEPQVQHFMTHDLGHRESSFSLRREFAQHAHAAKEGRN 811

Qy        626 AIIGLMVGGVVIATVIFITLVMLKKKQYTSIH-HGVVEVDAAVTP------EERHLSKMQ 678
                |  |: :   :|: : : | :   | |  | :|||  ||       ||: :  ||
Db        812 VYFTLSFAGIALMAAVFVGVAVAKWRTSRSPHAQGFIEVDQNVTTHHPIVREEKIVPNMQ 871

Qy        679 QNGYENPTYKFFE 691
              |||||||||:||
Db        872 INGYENPTYKYFE 884


RESULT 15
A4_BOVIN
```

```
ID   A4_BOVIN        STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             7.9%;  Score 287;  DB 1;  Length 59;
  Best Local Similarity   98.3%;  Pred. No. 1.2e-06;
  Matches   58;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        591 ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLK 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 59


Search completed: October  2, 2003, 13:59:43
Job time : 14 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:24 ; Search time 39 Seconds
(without alignments)
4611.863 Million cell updates/sec

Title: US-09-806-194-20
Perfect score: 3653
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3568	97.7	695	11	Q60496	Q60496 cavia sp. p
2	3535	96.8	695	11	P97487	P97487 mus musculu
3	3530.5	96.6	770	6	Q9TUI0	Q9tui0 sus scrofa
4	3423	93.7	695	13	Q9DGJ8	Q9dgj8 gallus gall
5	3382	92.6	751	13	Q9DGJ7	Q9dgj7 gallus gall
6	3209	87.8	693	13	Q98SG0	Q98sg0 xenopus lae
7	3185	87.2	695	13	Q98SF9	Q98sf9 xenopus lae
8	3098	84.8	747	13	Q91963	Q91963 xenopus. ap
9	2959.5	81.0	699	13	O57394	O57394 narke japon
10	2762.5	75.6	569	13	Q9PVL1	Q9pvl1 gallus gall
11	2630.5	72.0	607	11	Q99K32	Q99k32 mus musculu
12	2608	71.4	534	13	O93296	O93296 gallus gall
13	2568	70.3	780	13	O73683	O73683 tetraodon f
14	2524	69.1	738	13	Q90W28	Q90w28 brachydanio
15	2482.5	68.0	694	13	Q8UUR9	Q8uur9 brachydanio
16	2443.5	66.9	737	13	O93279	O93279 fugu rubrip
17	2334	63.9	612	13	Q9I9E7	Q9i9e7 brachydanio
18	1923	52.6	384	11	Q8BPC7	Q8bpc7 mus musculu
19	1757	48.1	695	4	Q13861	Q13861 homo sapien
20	1744.5	47.8	669	4	Q14662	Q14662 homo sapien
21	1735	47.5	695	11	Q64348	Q64348 mus musculu
22	1703	46.6	763	11	Q61482	Q61482 mus musculu
23	1699	46.5	751	11	Q60709	Q60709 mus musculu
24	1650	45.2	472	13	Q8UUS0	Q8uus0 brachydanio
25	1345.5	36.8	357	13	Q8UUI8	Q8uui8 brachydanio
26	1296.5	35.5	522	4	Q9BT36	Q9bt36 homo sapien
27	1085	29.7	218	11	Q8BPV5	Q8bpv5 mus musculu
28	1043.5	28.6	523	4	Q14594	Q14594 homo sapien
29	766	21.0	239	13	Q8UUI7	Q8uui7 brachydanio
30	678	18.6	136	6	P79307	P79307 sus scrofa
31	572	15.7	113	13	Q8JH58	Q8jh58 chelydra se
32	561	15.4	182	11	Q9CYS4	Q9cys4 mus musculu
33	478	13.1	97	6	Q28673	Q28673 oryctolagus
34	396.5	10.9	82	4	Q16014	Q16014 homo sapien
35	390.5	10.7	82	4	Q16019	Q16019 homo sapien
36	387.5	10.6	82	4	Q16020	Q16020 homo sapien
37	371	10.2	79	11	O35463	O35463 cricetulus
38	358.5	9.8	160	11	Q9QZ78	Q9qz78 cavia sp. p
39	330	9.0	208	11	Q8R0R7	Q8r0r7 mus musculu
40	234	6.4	49	6	O97917	O97917 bos taurus
41	196.5	5.4	727	5	Q95TG7	Q95tg7 drosophila
42	196.5	5.4	5303	5	Q9V628	Q9v628 drosophila
43	192.5	5.3	556	5	Q95S93	Q95s93 drosophila
44	192.5	5.3	1110	13	Q91255	Q91255 petromyzon
45	191.5	5.2	556	5	Q9V719	Q9v719 drosophila

ALIGNMENTS

RESULT 1
Q60496
ID Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative amyloid precursor protein.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 97.7%; Score 3568; DB 11; Length 695;
Best Local Similarity 97.7%; Pred. No. 6.1e-208;
Matches 679; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

```
Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||  |||||||||||||||||||||||||||:||||||||||||: ||||||
Db          1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWEPDPSGTK 60
```

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Qy        61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db        61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120

Qy       121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db       121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy       181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db       181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy       241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db       241 EADDDEDVEDGDEVEEEAEEPYEEATEKTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy       301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db       301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy       361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db       361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy       421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db       421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy       481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db       481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy       541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db       541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy       601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
Db       601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy       661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db       661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
```

RESULT 2
P97487
ID   P97487   PRELIMINARY;   PRT;   695 AA.
AC   P97487; P97942;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hippocampal amyloid protein.
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RA   Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 581-662 FROM N.A.
RC   STRAIN=129SV;
RA   Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA   Loring J.F., Goate A.M.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U84012; AAB41502.1; -.
DR   EMBL; U82624; AAB40919.1; -.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match 96.8%; Score 3535; DB 11; Length 695;
Best Local Similarity 97.1%; Pred. No. 6.1e-206;
Matches 675; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

```
Qy         1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db         1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy        61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db        61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy       121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db       121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy       181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db       181 GVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEE 240

Qy       241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
Db       241 EADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESVEEVVRVPTTAASTPDAA 300

Qy       301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Db       301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy       361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK 420
Db       361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHHVFNMLK 420

Qy       421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Db       421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy       481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
Db       481 EEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy       541 DDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Db       541 DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy       601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660
Db       601 GHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy       661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db       661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
```

RESULT 3
Q9TUI0
ID   Q9TUI0   PRELIMINARY;   PRT;   770 AA.
AC   Q9TUI0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Amyloid precursor protein.
OS   Sus scrofa (Pig).

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid Precursor Protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB032550; BAA84580.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   770 AA;  86961 MW;  5F7A1DCB2BCC583E CRC64;

  Query Match           96.6%;  Score 3530.5;  DB 6;  Length 770;
  Best Local Similarity  88.3%;  Pred. No. 1.3e-205;
  Matches  680;  Conservative    8;  Mismatches    7;  Indels   75;  Gaps    1;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              |||||||:|||||||||||||||:|||||||||||:|||||:|||||||||||:|:||||:||
Db          1 MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              ||| ||||||||||||||:|||||||||||||||||||| |||||:|| | :|||||:||
Db         61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
              |||||||||||||||:|||||||||||||||||||||||||:|||||||||||||:|||:|||
Db        181 GVEFVCCPLAEESDNIDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVADVEEE 240

Qy        241 EADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR------------ 288
              ||:|||||||||||||||||||||||||||||||||||||||||||||
Db        241 EAEDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy        289 ------------------------------------------------------------ 288

Db        301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVMSQSLLKTTQEPLPQD 360

Qy        289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
                 :|||||:|||||.||||:||||||.||||:|||||||||||||||||:| |||
Db        361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy        346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
              |||||||||||||||'|||||||||||||||||||||||||||||||||||||, ||||
Db        421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy        406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
              |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy        466 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 525
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTET 600

Qy        526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTIRPGSGLTN 585
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTIRPGSGLTN 660

Qy        586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITL 645
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy        646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770


RESULT 4
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match           93.7%;  Score 3423;  DB 13;  Length 695;
  Best Local Similarity  93.8%;  Pred. No. 3.7e-199;
  Matches  654;  Conservative   17;  Mismatches   22;  Indels    4;  Gaps    3;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| ||||||||  |||||||:|||||||||||||||||:|||||||||||:|:||||:||
Db          1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
              |||||.|||||||||||||||||||||||||||||||| ||  ||| |:|||||:||
Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              |||||:|||||||| |||:|||||||||||||||:||||| ||||||||||||:|||
Db        121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238
              ||||||||||||||:|:|||:|||||||||| ||||||:|||||    :||:  ||
Db        181 GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVE 240

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
              :|:||||  ||:||||: || || |||||||||||||||||||||||||||||||||||||
Db        241 DEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVRVPITAASTPD 298

Qy        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358

Qy        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM 418
              |||||||||||||||||||||||||||||||||||||:|||||||||| ||||||||||
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Db        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNM 418

Qy        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478

Db        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPA 478

Qy        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF 538

Db        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEF 538

Qy        539 SLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA 598

Db        539 SLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDA 598

Qy        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658

Db        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658

Qy        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Db        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695


RESULT 5
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match           92.6%;  Score 3382;  DB 13;  Length 751;
  Best Local Similarity  86.7%;  Pred. No. 1.2e-196;
  Matches  653;  Conservative   18;  Mismatches   22;  Indels   60;  Gaps    4;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db          1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Db         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG 120

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db        121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR 180

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238

Db        181 GVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVE 240

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------- 288

Db        241 DEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETG 298

Qy        289 ----------------------------------------------VPTTAASTPDAVDK 302

Db        299 PCRAMISRWYFDVAEGKCAPFFYGGCGGNRNNFDSEEYCMAVCGSVLPTTAASTPDAVDK 358

Qy        303 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 362

Db        359 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQE 418

Qy        363 KVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKY 422

Db        419 KVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKY 478

Qy        423 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEE 482

Db        479 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEE 538

Qy        483 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDD 542

Db        539 IQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEFSLDD 598

Qy        543 LQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH 602

Db        599 LQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDAEFRH 658

Qy        603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVE 662

Db        659 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE 718

Qy        663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

Db        719 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751


RESULT 6
Q98SG0
ID   Q98SG0      PRELIMINARY;      PRT;   693 AA.
AC   Q98SG0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein A.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298150; CAC37193.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
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DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   693 AA;  78568 MW;  CAF1DF655C1AB653 CRC64;

  Query Match             87.8%;  Score 3209;  DB 13;  Length 693;
  Best Local Similarity   87.7%;  Pred. No. 3.4e-186;
  Matches  611;  Conservative   36;  Mismatches   44;  Indels    6;  Gaps    4;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| : |:::    | ||||| ||| ||||||||||||:|||.|||:||||::  |||:
Db          1 MLPHITLLVLTV-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               :| ||||||||||||||||||||||||||||||||||:|:||:|| |||:   | |::|||!
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||||||||||||||||||||:||||||||||||| :|||. :||::||||| ||| ||
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFR 179

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVE 238
              ||||||| ||||:: ||||| ||||  ||||||  || | |:|| .|     | ||| |:|
Db        180 GVEFVCCPSAEESESFDSADA-EDDSDAWWGGADADYVDRSDDKAVEAQPDEEEEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPD 298
              ||| |||||   |||: ||| |||||:|||||||||||||:||||:.||||| ||| |||
Db        239 EEETDDDED--DGDEAEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRVPATAASTPD 296

Qy        299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ 358
              |||||| | |||||   | ||||||:||:|||:||:|||||||||||||||||||||||||
Db        297 AVDKYLENPNDENEHDRFLKAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQ 356

Qy        359 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNM 418
              |||||||||||:||||||||||||||||||||||||||||:||||||||| |||||||||
Db        357 HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNM 416

Qy        419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA 478
              ||||||||||||||||||||||||||||||||||||||||||||| ||||| |||| |||
Db        417 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPA 476

Qy        479 VAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEF 538
              |||||||||||| |||| ||||::::||:| |:||:||||||.:|||||:|||:|:||
Db        477 VAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEF 535

Qy        539 SLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA 598
              :::|:||||||||:||||||||||||||||||||||:|||||||||||||||||||||:
Db        537 NIEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDS 596

Qy        599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHH 658
              |:| |: |||||||| ||:||:||||||||||||||||||:  ||||.|||:| |:|||
Db        597 EYRHDTAYEVHHQKLVFFAEEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHH 656

Qy        659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||:|||||:||||:||||||||.|||||||:||
Db        657 GVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 693

RESULT 7
Q98SF9
ID   Q98SF9      PRELIMINARY;      PRT;    695 AA.
AC   Q98SF9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-amyloid precursor protein B.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298151; CAC37194.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   695 AA;  78803 MW;  DC14EB02AFB0204A CRC64;

  Query Match             87.2%;  Score 3185;  DB 13;  Length 695;
  Best Local Similarity   87.1%;  Pred. No. 9.6e-185;
  Matches  608;  Conservative   39;  Mismatches   45;  Indels    6;  Gaps    5;

Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
              ||| : ||:| |   | |||| ||| ||||||||||||:||||||||||||::| ||||
Db          1 MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK 59

Qy         61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
               || ||||||||||||||||||||||||||||||||||:|:||||:   | |:|:||||
Db         60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy        121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
              ||||| ||||||||||||||||:|||||||||||||||||||:||||  :|:|||||||||||
Db        120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR 179

Qy        181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAEVE 238
              ||||||| ||||:: ||||| ||||||||||| || | |:|| ||    ||||| |||
Db        180 GVEFVCCPTAEESESFDSADA-EDDSDVWWGGADADYVDRSDDKAVEAQPEEEEEVVEVE 238

Qy        239 EEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR-VPTTAASTP 297
              |||||| |::|||| ||| ||||||||||||||||||||||||||||||| || || |||
Db        239 EEEADD-DEDDGDETEEEPEEPYEEATERTTSIATTTTTTTESVEEVVRAVPATAVSTP 297

Qy        298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
              ||||||| | ||||| | |||||||| ||||:|||:||||||||||||||||||||||||
Db        298 DAVDKYLENPNDENEHDRFLKAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVI 357

Qy        358 QHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFN 417
              ||||||||||||||||||||||||||||||| ||||||:||||||||||| ||||||||||
Db        358 QHFQEKVESLEQEAANERQQLVETHMARVEATLNDRRRIALENYITALQADPPRPRHVFN 417

Qy        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
              |||||||||||||||||||||||||||||||||||||||||||| |||||  |||| ||
Db        418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVP 477

Qy        478 AVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGE 537
              |||||||||||| ||:|||||:::||:|: |:|||||||||||:|||||||||||||:|:
Db        478 AVAEEIQDEVDELFQKEQNYSDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGE 537

Qy        538 FSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMD 597
              |:::|||||||||||:|||||||||||||||||||||||||||||||||:|:||||||||
Db        538 FNVEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKREEISEVKMD 597

Qy        598 AEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIH 657
              :|:||: |||||||||||||:||||||||||||||||||||||||:|||||||||||:||
Db        598 SEYRHDAAYEVHHQKLVFFADEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIH 657

Qy        658 HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||||||||||||||||:||||||||||||||||||||
Db        658 HGVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 695

RESULT 8
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Q91963
ID   Q91963      PRELIMINARY;      PRT;   747 AA.
AC   Q91963;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   APP747.
GN   APP747.
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93129227; PubMed=1282805;
RA   Okado H., Okamoto H.;
RT   "A Xenopus homologue of the human beta-amyloid precursor protein:
RT   developmental regulation of its gene expression.";
RL   Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR   EMBL; S52417; AAB24853.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   747 AA;  84893 MW;  A75E81885681D948 CRC64;

  Query Match             84.8%;  Score 3098;  DB 13;  Length 747;
  Best Local Similarity   80.9%;  Pred. No. 1.9e-179;
  Matches  597;  Conservative   35;  Mismatches   42;  Indels   64;  Gaps    5;

Qy         17 ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQE 75
              ||||  ||| |||||||:|||   |||||:||||.:::|  |   || ||||||||||
Db         15 ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE 71

Qy         76 VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF 135
              ||||||||||||||||||||||||||||:|||||:  | |:|||||||||||||||||||
Db         72 VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF 131

Qy        136 LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN 195
              |||||||:|||||||||||||:||||' :||:|:|||:|||||||||||:||| |||::
Db        132 LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEESES 191

Qy        196 VDSADAEEDDSDVWWGGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDDEDDEDGDE 253
              ||||| ||| |||||||| || | |:|| ||    :|||| .|||| |||    ||||
Db        192 FDSADAAEDDCDVWWGGADADYVDRSDDKAVEAQPDEEEEVVEVEEEEETDDDED--DGDE 249

Qy        254 VEEEAEEPYEEATERTTSIATTTTTTTESVEEVVR---------------------- 288
              ||| ||||||||||||||||||||||||||||||
Db        250 AEEEPEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYYDVIE 309

Qy        289 ------------------------------VPTTAASTPDAVDKYLETPGDENEHAHFQ 317
                                           :| |||||||||||||: | ||||  :
Db        310 SKCAQFIYGGCGGNRNNFESDDYCMAVCGSVIPATAASTPDAVDKYLENPNDENEHDRFL 369

Qy        318 KAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQ 377
              ||||||| ||||:||:||:|||||||||||||||||||||||||||||||||:||| :|||
Db        370 KAKERLEGKHREKMSEVMKEWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ 429

Qy        378 LVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 437
              ||||||||||||||||||:|||||||||| |||||||||||||||||||||||||||||

Db        430 LVETHMARVEAMLNDRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHF 489

Qy        438 EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNY 497
              |||||||||:|||||||||||||||||| |||||| |||| |||||||||||||| |||||
Db        490 EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAVAEEIQDEVDELFQKEQNY 549

Qy        498 SDDVLANMISEPRISYGNDALMPSLTEIKTTVELLPVNGEFSLDDLQPWHSFGADSVPAN 557
              |||::::||:|: |:|||||||||||:|||||||||:|||:::|||||||| ||||||
Db        550 SDDMVSNMVSDHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPWHSFGVDSVPAN 609

Qy        558 TENEVEPVDARPAADRGLTIRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA 617
              |||||||||||||||||||||||||||||||||||||||||:|:|||: ||||||||||
Db        610 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHDTAYEVHHQKLVFFA 669

Qy        618 EDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKM 677
              |:|||||||||||||||||||| ||||||||||||:|||||||||||||||||||:||
Db        670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHHGVVEVDAAVTPEERHLTKM 729

Qy        678 QQNGYENPTYKFFEQMQN 695
              ||||||||||||||||||
Db        730 QQNGYENPTYKFFEQMQN 747


RESULT 9
O57394
ID   O57394      PRELIMINARY;      PRT;   699 AA.
AC   O57394;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   EL amyloid precursor protein 699.
GN   EL APP699.
OS   Narke japonica (Electric ray).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Torpediniformes; Narcinoidei; Narkidae; Narke.
OX   NCBI_TaxID=62965;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Electric lobe;
RX   MEDLINE=98129705; PubMed=9461486;
RA   Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA   Suzuki T.;
RT   "cDNA isolation of Alzheimer's amyloid precursor protein from
RT   cholinergic nerve terminals of the electric organ of the electric
RT   ray.";
RL   Biochem. J. 330:29-33(1998).
DR   EMBL; AB005544; BAA24230.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   699 AA;  78879 MW;  952915C309D50E5C CRC64;

  Query Match             81.0%;  Score 2959.5;  DB 13;  Length 699;
  Best Local Similarity   80.7%;  Pred. No. 4.4e-171;
  Matches  568;  Conservative   58;  Mismatches   59;  Indels   19;  Gaps    8;

Qy          2 LPG-LALLLAAWTA-------RALEVPTDGNAGLL-AEPQIAMFCGRLNMHMNVQNGKW 52
              ||| | :|||||  |        |||||||| |||| ||||||||:||||:||| |||
Db          5 LPGRLGMLLLAAAAALVLAPLCRALEVPTDGGAGLLAAEPQIAMFCGKLNMHVNVQTGKW 64

Qy         53 DSDPSGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKTHPHFV 112
              |||||| ||  ||||||:|||||||:|||||||||||:|||||||:|||||| ||| |
Db         65 VSDPSGTNTCFGTKEGILRYCQEVYPDLQITNVVEANQPITIQNWCKKGRKQCKGHPHIV 124

Qy        113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
              :|||||||||||||||||||||||:|:|| ||:||:|||||||| :|  |||||||||
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Db        125 VPYRCLVGEFVSDALLVPDKCKFLHREKMDTCESHLYWHTVAKETCGDKIMNLHDYGMLL 184

Qy        173 PCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEE 232
              |||||:|||||||||||: |:|:| :|| | :|:|||||||  | ||:|| |: | |  ||
Db        185 PCGIDEFRGVEFVCCPIPEENDKIDS-DMDEEDSDVWWGGDDADYADGG-DKTV----EE 238

Qy        233 EVAEVEEEEADDDEDDEDGDEVEEE-AEEPYEEATERTTSIATTTTTTTESVEEVVRVPT 291
              :  | |||| : | ||||: |::::|  |: ||: || ||||  :|||||||::|||| |||
Db        239 KPIEEEEEEDESDIDDEDDDDLDDEVVEDQYEDPTEHTIS---STTTTIEAIEEVVRVPT 295

Qy        292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
              |||||||:|||||||| |:|||:|||||||:|||||: ||::.|||||: ||| |||||
Db        296 TAASTPDAVDKYLETPGDENEHAYFQKAKERLEAKHRERMSKIMREWEEAERQAKNLPKA 355

Qy        352 DKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQAVPPR 411
              |||||| ||| |:|||.|||:||||||||||||||||.||||.:|||||: || | |||
Db        356 DKKAVIQRFQEMVESLEQEAASERQQLVETHMARVEAMLNDRRRIALENYIAALQADPPR 415

Qy        412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLS 471
              |||| | |||| |:||| ||||||||:||| |||:||||:|||||| || ||||||||
Db        416 PRHVLNALKKYSRAEQKDRQHTLKHFDHVRAVDPEKAAQIKSQVMTHLHVIDERMNQSLS 475

Qy        472 LLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVEL 531
              ||| ||:|||||||||| |||:|:|| ||::|| :|: ||||:|||:|+|:|||||:||
Db        476 LLYKVPSVAEEIQDEVDELLQRERSYMDDMMANSVSDTRISYGNDALVPSLSETKTTIEL 535

Qy        532 LPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI 591
              |. :||| |||||| | |  :|:|||||||||||||:|| |||||||||||| :|||||
Db        536 LPDDGEFILDDLQPPHPFVIESIPANTENEVEPVDARPAPDRGLTTRPGSGLTGIKTEEI 595

Qy        592 SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKK 651
              :|:||: ||: |||||||||||||| :|:|||||||.||||-|||||||| |||||||.|
Db        596 AELKMETEFQQDSGYEVHHQKLVFFPKDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 655

Qy        652 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||||||||||||||||||||||||||||||||||||||
Db        656 QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 699


RESULT 10
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             75.6%;  Score 2762.5;  DB 13;  Length 569;
  Best Local Similarity   93.4%;  Pred. No. 2.8e-159;
  Matches  534;  Conservative   14;  Mismatches   19;  Indels    5;  Gaps    4;

Qy        126 ALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFV 185
              |||||||| |||||||||||||||||||||||:|||| |||||||| ||||||||||||
Db          1 ALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLSCGIDKFRGVEFV 60

Qy        186 CCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVE--VAEEEEVAEVEEEEAD 243
              |||:|||||:|||||:|||||||||| |:||||:|||||    |:|||  ||:|:||
Db         61 CCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDDKVVEEQPEEDEELTVVEDEDAD 120

Qy        244 DDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAVDKY 303
              || ||:|||| || || |||||||||||||||:|||||||||||||:|||||||| ||||
Db        121 DD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTESVEEVVRVPTIAASTPDVVDKY 178

Qy        304 LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEK 363
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 LETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEK 238

Qy        364 VESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYV 423
              |||||||||||||||||||||||||||||||:|||||||| ||||||||||||||||||
Db        239 VESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKYV 298

Qy        424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI 483
              |||:|||||||||||||||||||:| |||||||||||||||||| |:|||||||||||
Db        299 RAEQKDRQHTLKHFEHVRMVDPKKAVQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEEI 358

Qy        484 QDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDL 543
              |||||||||||||||||||||||||||||||||||||:|||||||||||||| ||||||||
Db        359 QDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPTLTETKTTVELLPVVGEFSLDDL 418

Qy        544 QPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHD 603
              |||| || |||||||||||||||||||||||||||||||||||:||||:||||||||||
Db        419 QPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDAEFRHD 478

Qy        604 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEV 663
              |||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db        479 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIANVIVITLVMLKKKQYTSIHHGVVEV 538

Qy        664 DAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||| ||||||||||||||||||||||||
Db        539 DAAVTP-ERHLSKMQQNGYENPTYKFFEQMQN 569


RESULT 11
Q99K32
ID   Q99K32      PRELIMINARY;      PRT;   607 AA.
AC   Q99K32;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical 68.4 kDa protein (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005490; AAH05490.1; -.
DR   HSSP; P05067; 1AAP.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
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DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
FT   NON_TER       1       1
SQ   SEQUENCE   607 AA;  68391 MW;  BF802214CBA7D172 CRC64;

  Query Match           72.0%;  Score 2630.5;  DB 11;  Length 607;
  Best Local Similarity  85.5%;  Pred. No. 3e-151;
  Matches  519;  Conservative    4;  Mismatches    9;  Indels   75;  Gaps    1;

Qy        164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSED 223
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||.| ||
Db          1 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDSVDSADAEEDDSDVWWGGADTDYADGGED 60

Qy        224 KVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESV 283
              |||||||||||||:|||||||||||| ||||||||||||||:|||||.|||| |||||'|||:|
Db         61 KVVEVAEEEEVADVEEEEADDDEDVEDGDEVEEEAEEPYEEATERTTSTATTTTTTTESV 120

Qy        284 EEVVR---------------------------------------------------------- 288
              |||||
Db        121 EEVVREVCSEQAETGPCRAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGS 180

Qy        289 --------------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHR 328
                                  :|.||||||||||||| |||||.|||||-|||:|||||.|
Db        181 VSTQSLLKTTSEPLPQDPDKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHR 240

Qy        329 ERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEA 388
              |||'||||||'|||||'|||||'||||||||||'|||||.|||||:|||||:|||||| ||
Db        241 ERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEA 300

Qy        389 MLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKA 448
              |||||||||||||:|||||||:||| ||||||||.|||||||||| |||||.||| |||
Db        301 MLNDRRRLALENYITALQAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKA 360

Qy        449 AQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISE 508
              |||||:|||||||||||:|||||||||'|||||||||||||||:|||.|||||''|||||
Db        361 AQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISE 420

Qy        509 PRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDAR 568
              :|||||||||||||||||||||||||||||||'|||||.| || .|||||''||||.:|||||
Db        421 PRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDAR 480

Qy        569 PAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 628
              |||||||||||||||||||||||||||||:| ||||:|| |.|||'||||||.||| ||
Db        481 PAADRGLTTRPGSGLTNIKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAEDVGSNKGAII 540

Qy        629 GLMVGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYK 688
              |||||||||||| ||||||||||||||||||||||||||||||| |||'|||||| ||
Db        541 GLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYK 600

Qy        689 FFEQMQN 695
              |||||||
Db        601 FFEQMQN 607


RESULT 12
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.

RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match           71.4%;  Score 2608;  DB 13;  Length 534;
  Best Local Similarity  94.6%;  Pred. No. 5.9e-150;
  Matches  505;  Conservative   13;  Mismatches   12;  Indels    4;  Gaps    3;

Qy        164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSED 223
              ||||||:|||||||||||||||||||||||||:||||||:||||||||||| |||||||:|
Db          3 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADYADGSDD 62

Qy        224 KVVE--VAEEEEVAEVEEEEADDDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTE 281
              ||||    |:||: ||:|:|||| ||:|||: || || |||||||||:|||||||||
Db         63 KVVEEQPEEDEELTVVEDEDADDD-DDDDGDEI-EETEEEYEEATERTTSIATTTTTTTE 120

Qy        282 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 180

Qy        342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENY 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        181 ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRIALENY 240

Qy        402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ITALQTVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 300

Qy        462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 521
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IYERMNQSLSFLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPS 360

Qy        522 LTETKTIVELLPVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGS 581
              |||||||||||||:|||||||||||| || ||||||||||||||||||||||||||||||
Db        361 LTETKTTVELLPVDGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGS 420

Qy        582 GLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 641
              ||||:||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GLTNVKTEEVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 480

Qy        642 FITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              |||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VITLVMLKKKQYTSIHHGVVEVDAAVIPEERHLSKMQQNGYENPTYKFFEQMQN 534


RESULT 13
O73683
ID   O73683      PRELIMINARY;      PRT;   780 AA.
AC   O73683;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Tetraodon fluviatilis (Puffer fish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC       WITH XI1-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC       RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC       NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC       PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
CC       BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    780       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                HOMOLOG.
FT   CHAIN       682    724       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    732       POTENTIAL.
FT   DOMAIN      733    780       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      323    382       BPTI/KUNITZ INHIBITOR.
FT   SITE        769    772       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    327    378       BY SIMILARITY.
FT   DISULFID    336    361       BY SIMILARITY.
FT   CARBOHYD    560    560       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   780 AA;  88238 MW;  60071BE94520191D CRC64;

  Query Match             70.3%;  Score 2568;  DB 13;  Length 780;
  Best Local Similarity   65.3%;  Pred. No. 2.6e-147;
  Matches  512;  Conservative   71;  Mismatches   95;  Indels  106;  Gaps   10;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
              |||:|| :  : |||' : |||||||:||||:: ||:|:::||: ||||:|:|| ::
Db          8 LLLVAAASTLAAEVPTDVSMGLLAEPQVAMFCGKINMHINVQSGKWEPDPSGTKSCIGTK 67

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
              |||||||||||||||||||||||||:|:||||:|||:::|  ' |:.|||||: |||||
Db         68 EGILQYCQEVYPELQITNVVEANQPVSIQNWCKKGRKQCRSHMHIVVPYRCLVGEFVSDA 127

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
              |||||||||||||||: '|:|||-||||||:| ::: |||||'||||||||:. ||||.
Db        128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVEFVC 187

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS----------EDKVVEVAEEE 232
              || ||   ::|| : : ||||||||||| ||:| |               |:|  ||
Db        188 CP-AEAERDMDSTEKDADDSDVWWGGADNDYSDNSMVREPEPAEQQEETRPSVVEEEEEG 246

Qy        233 EVAEVEEEE----------------ADDDEDDEDGDEVEEEAEEPYEEATERTTSIA 273
              |||: ::||                  |||:|::|| |||:   |    :| | |||:|
Db        247 EVAQEDDEEEEEVLDTDQDGDGEEDHEAADDEEEEEDVDEIDAFGESDDVDADEPTTNVA 306

Qy        274 ---TITTTTTESVEEVVR---------------------------------------- 288
                  ||||||||||||||
Db        307 MTTTTTTTTTESVEEVVRMFCWAHADTGPCTASMPSWYFDAVDGRTMYELMYGGCGGNMN 366

Qy        289 --------------VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQ 333
                           |||   |:|||| |||| ||||||||||||| ||||||||||
Db        367 NFESEEYCLSVCSSVVPTDMPSSPDAVDHYLETPADENEHAHFQKAKESLEAKHRERMSQ 426

Qy        334 VMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDR 393
              ||||:|||||||||||:|||| ||| |||||':|||||:|||||||||||||:|||
Db        427 VMREWEEAERQAKNLPRADKKIVIQRFQEKVEALEQEAASERQQLVETHMARVEALLNDR 486

Qy        394 RRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRS 453
              ||||||||:|||  ||||||||::|||||||||||||||||||||||||||||||||
Db        487 RRLALENYLTALQQDPPRPRHVFSLLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRP 546

Qy        454 QVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISY 513
              ||:|||||| |||||||  ||| || ||::||':| ||||:||      |||: :: |:||
Db        547 QVLTHLRVIEERMNQSLGLLYKVPGVADDIQDQV-ELLQREQAEMAQQLANLQTDVRVSY 605

Qy        514 GNDALMPSLTETKTTVELLPVNGEFSLDDLQPWH--SFGADSVPANTENEVEPVDARPAA 571
              |||||||       :|||   | :|  :   |  ||       ||||:|||||:||
Db        606 GNDALMPDQELGDGQADLLP--QEDTLGGVGFVHPESFN----QLNTENQVEPVDSRPTF 659

Qy        572 DRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLM 631
              :||: |||   :|    | : |::|: | |  : ||||||||||||||:|||||||||
Db        660 ERGVPTRP---VTGKSMEAVPELRMETEDRQSTEYEVHHQKLVFFAEDVGSNKGAIIGLM 716

Qy        632 VGGVVIATVIFITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
              |||||||||| ||||||:|||||||||::|||||||||||||||||||||||||||||
Db        717 VGGVVIATVIVITLVMLRKKQYTSIHHGIIEVDAAVTPEERHLSKMQQNGYENPTYKFFE 776

Qy        692 QMQN 695
              ||||
Db        777 QMQN 780


RESULT 14
Q90W28
ID   Q90W28      PRELIMINARY;      PRT;   738 AA.
AC   Q90W28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid precursor protein.
GN   APPA OR APP.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Expression analysis of zebrafish app.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389401; AAK64495.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
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DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   738 AA;  83577 MW;  AF480F6D308FD298 CRC64;

  Query Match             69.1%;  Score 2524;  DB 13;  Length 738;
  Best Local Similarity   66.3%;  Pred. No. 1.1e-144;
  Matches  500;  Conservative   79;  Mismatches   91;  Indels   84;  Gaps   14;

Qy          5 LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCID 64
Db          6 LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPDPSGSKSCIG 65

Qy         65 TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVS 124
Db         66 NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS 125

Qy        125 DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF 184
Db        126 DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF 185

Qy        185 VCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADD 244
Db        186 VCCP-ADAGKESESAAVEEDDSDVWWGGAEADYTENSMTR--DAAAEPAVLE-DDEDADE 241

Qy        245 DED-DEDGD-----EVEEEAEEPYEEATERTT-SIATTTTTTTESVEEVVR--------- 288
Db        242 EEDEDQDGDGDRDEKIEEEEEE--EERTQSTSAALTSTTTTTTESVEEVVREVCFASAET 299

Qy        289 ---------------------------------------------VPTTAASTPDAVD 301
Db        300 GPCRAMLSRWYYVREERRCAPFIYGGCGGNRNNFESEEYCLSVCSGVLPTPSSSPPDAVD 359

Qy        302 KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQ 361
Db        360 RYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAKSLPRNDKKAVIQHFQ 419

Qy        362 EKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLKK 421
Db        420 EKVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQADPPRPRHVFSLLKK 479

Qy        422 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAE 481
Db        480 YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVAD 539

Qy        482 EIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLD 541
Db        540 DIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFG 595

Qy        542 DLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFR 601
Db        596 FIHP-ESFN----QPNTHNQVEPVDARPVPDLDLATRPVSGL---KPDDIPELRMEAEER 647

Qy        602 HDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGVV 661
Db        648 HS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIVITLVMLRKKQYTSIHHGII 704

Qy        662 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db        705 EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 738

RESULT 15
Q8UUR9
ID   Q8UUR9      PRELIMINARY;      PRT;   694 AA.
AC   Q8UUR9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Putative membrane protein.
GN   APPB.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11862463;
RA   Musa A., Lehrach H., Russo V.E.A.;
RT   "Distinct expression patterns of two zebrafish homologues of the human
RT   APP gene during embryonic development.";
RL   Dev. Genes Evol. 211:563-567(2001).
DR   EMBL; AJ315639; CAC85736.1; -.
DR   ZFIN; ZDB-GENE-020220-1; appb.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   694 AA;  79228 MW;  2B03382D411162DC CRC64;

  Query Match             68.0%;  Score 2482.5;  DB 13;  Length 694;
  Best Local Similarity   67.7%;  Pred. No. 3.3e-142;
  Matches  476;  Conservative   98;  Mismatches   98;  Indels   31;  Gaps    9;

Qy          7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK 66
Db          9 LLLMLTTLSLAIEVPSDDSVGLLAEPQVAMFCGKLNMHINVQSGKWEPDPTGTKSCISTK 68

Qy         67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126
Db         69 EGILKYCQEVYPDLQITNVVEANQPVSIQNWCKMGRRQCRSHTHIVVPYRCLVGEFVSDA 128

Qy        127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186
Db        129 LLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVC 188

Qy        187 CPLAEESDNVDSADAEEDDSDVWWGGADTDYADGS--EDKVV-----EVAEEEEVAEVEE 239
Db        189 CPMEEQKD-LDSEEQEEANSDVWWGGAETEYTDASVLKEQVTAKPDPAVTEDDEDLNNEE 247

Qy        240 EADDDEDDEDGDEVEEEAEE-----PYEEATERTTSIA--TTTTTTTESVEEVVRVPTT 292
Db        248 EEVWDNDEDGDGEDDEDEEDDDEDIIDEQDTSEQTSNIAMTTTTTTTTESIEEVVRVPTM 307

Qy        293 AASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKAD 352
Db        308 APSPADAVDRYLEAPGDMNEHMRFQKAKESLEAKHREKMSEVMREWEEAERQAKNLPRAD 367

Qy        353 KKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRP 412
Db        368 KKTIIQRFQEKVESLEKEAAGERQQLVETHMARVEALLNDRRRQALESYLSSLQSDQPRP 427

Qy        413 RHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSL 472
Db        428 RQVLNLLKKYIRAEQKDRQHTLKHFEHVREVDPKKASQIRPFVMTHLRVIEERMNQSLGY 487

Qy        473 LYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELL 532
Db        488 LYKVPQVANDIQDQVAVLVQRDQAEVTQQLSSLQSKMRVSYGNDALMPDLPDSTTPLDNL 547

Qy        533 PVNGEFSLDDLQPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEIS 592
Db        548 PPEQD-GLGFIHP-ESFN----QANTDNHVEPVDARPIPERGLPTRP----------EIP 591

Qy        593 EVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQ 652
Db        592 KVRLDIEERHNAGYDVRDKRLMFLAEDMGSNKGAIIGLMVGGVVIATVIVITLVMLRKKQ 651
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Qy        653 YTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
              ||.| |||:|||| |||||:||:||?|||||||:|||.| |||
Db        652 YTSIHHGVIEVDAAVTPEERHLAKMQQNGYENPTYKPFEQMQN 694

Search completed: October 2, 2003, 14:02:40
Job time : 41 secs
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